

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:10:15 ; Search time 46 Seconds
(without alignments)
6365.237 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSSFPKFVSTFAIFPLSM.....FELGSSRNNDLGAQYF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3991	83.6	772	16 Q9RB71	Q9rb71 chlamydia p
2	1923	40.3	926	16 Q823W9	Q823w9 chlamydia p
3	1915	40.1	926	2 P71135	P71135 chlamydia p
4	1805	37.8	942	16 Q823X1	Q823x1 chlamydia p
5	1748.5	36.6	866	16 Q823X0	Q823x0 chlamydia p
6	1667	34.9	841	16 Q822Q5	Q822q5 chlamydia p
7	1656.5	34.7	839	2 P77792	P77792 chlamydia p
8	1641.5	34.4	847	2 P71132	P71132 chlamydia p
9	1604.5	33.6	846	2 P71133	P71133 chlamydia p
10	1410.5	29.5	1011	16 Q823X5	Q823x5 chlamydia p
11	1237	25.9	602	2 Q8VU49	Q8vu49 chlamydia p
12	1219.5	25.5	601	2 Q8VL57	Q8vl57 chlamydia p
13	1186.5	24.9	843	16 Q823X3	Q823x3 chlamydia p
14	1175	24.6	700	2 Q8VU50	Q8vu50 chlamydia p
15	1172.5	24.6	581	2 Q8VU48	Q8vu48 chlamydia p
16	1161.5	24.3	843	16 Q823X2	Q823x2 chlamydia p

17	1116	23.4	868	16 Q823X4	Q823x4 chlamydia p
18	1103	23.1	591	16 Q7VQA1	Q7vqa1 chlamydia p
19	1020.5	21.4	445	16 Q7VQ99	Q7vq99 chlamydia p
20	1017.5	21.3	445	16 Q9RB67	Q9rb67 chlamydia p
21	935.5	19.6	649	2 P71134	P71134 chlamydia p
22	921	19.3	354	16 Q7VQA0	Q7vqa0 chlamydia p
23	916	19.2	359	16 Q9JSK6	Q9jsk6 chlamydia p
24	847	17.7	846	2 Q84FU0	Q84fu0 chlamydia p
25	843	17.7	846	2 Q84FU5	Q84fu5 chlamydia p
26	843	17.7	846	2 Q84FU2	Q84fu2 chlamydia p
27	841	17.6	846	2 Q84FU1	Q84fu1 chlamydia p
28	840	17.6	846	2 Q84FU4	Q84fu4 chlamydia p
29	838	17.6	846	2 Q84FU3	Q84fu3 chlamydia p
30	835	17.5	846	2 Q83TT8	Q83tt8 chlamydia p
31	834	17.5	846	2 Q83U50	Q83u50 chlamydia p
32	833	17.4	846	2 Q84FT9	Q84ft9 chlamydia p
33	832	17.4	846	2 Q84FT8	Q84ft8 chlamydia p
34	831	17.4	846	2 Q84FT7	Q84ft7 chlamydia p
35	821	17.2	494	16 Q9RB68	Q9rb68 chlamydia p
36	792	16.6	427	16 Q9RB70	Q9rb70 chlamydia p
37	768	16.1	177	16 Q7VQA2	Q7vqa2 chlamydia p
38	768	16.1	186	16 Q9RB72	Q9rb72 chlamydia p
39	717	15.0	934	16 Q824E6	Q824e6 chlamydia p
40	676.5	14.2	1537	16 Q821X9	Q821x9 chlamydia p
41	673	14.1	941	16 Q823Y1	Q823y1 chlamydia p
42	658.5	13.8	981	16 Q823X6	Q823x6 chlamydia p
43	655	13.7	1795	16 Q824E7	Q824e7 chlamydia p
44	644.5	13.5	936	16 Q823Y2	Q823y2 chlamydia p
45	614.5	12.9	980	2 Q84FU6	Q84fu6 chlamydia p

ALIGNMENTS

RESULT 1

Q9RB71	Q9RB71	PRELIMINARY;	PRT;	772 AA.
AC	Q9RB71;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Pmp 3 (Outer membrane protein 5).			
GN	PMP 3 2 OR CPB0018.			
OS	Chlamydia pneumoniae (Chlamydophila pneumoniae).			
OC	Bacteria: Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.			
OX	NCBI_TaxID=83558;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=J138;			
RX	MEDLINE=20330349; PubMed=10871362;			
RA	Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,			
RA	Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;			
RT	"Comparison of whole genome sequences of Chlamydia pneumoniae J138			
RL	from Japan and CWL029 from USA."			
RL	Nucleic Acids Res. 28:2311-2314(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-TW-183;			
RA	Geng M.M., Schuhmacher A., Muehlhofer I., Bensch K.W., Schaefer K.P.,			
RA	Schneider S., Pohl T., Essig A., Marre R., Melchers K.;			
RT	"The genome sequence of Chlamydia pneumoniae TW183 and comparison with			
RL	other Chlamydia strains based on whole genome sequence analysis."			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.			
DR	EMBL; AF002545; BAA98226.1; -.			
DR	EMBL; AB017157; AAP97951.1; -.			
DR	PIR; H86492; H86492.			
DR	InterPro; IPR006315; Autotransport.			
DR	InterPro; IPR005546; Autotransporter.			
DR	InterPro; IPR003368; Chlamydia_PMP.			
DR	Pfam; PF03797; Autotransporter; 1.			
DR	Pfam; PF02415; Chlamydia_PMP; 1.			
DR	TIGRFAMs; TIGR01414; autotrans_bar1; 1.			
DR	TIGRFAMs; TIGR01376; POMP_repeat; 6.			

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SQ SEQUENCE 772 AA; 82931 MW; 484FC56D635801EB CRC64;
Query Match 83.6%; Score 3991; DB 16; Length 772;
Best Local Similarity 99.9%; Pred. No. 6.8e-175;
Matches 771; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 157 LRFKNTSTNGGALTAKTLSTLTGTTMSALFSENTSSKKGGAIGTSDALITITNGQGVSF 216
DB 1 MLFKNSTNGGALTAKTLSTLTGTTMSALFSENTSSKKGGAIGTSDALITITNGQGVSF 60
QY 217 SDNTSSDGAIFTEASVTISNNAKVSFIDNKVTGASSTTGDMSGGAICAYKSTSTDKV 276
DB 61 SDNTSSDGAIFTEASVTISNNAKVSFIDNKVTGASSTTGDMSGGAICAYKSTSTDKV 120
QY 277 TLGNQMLLFNNSTTAGGAIYKKLELASSGLTLFRNSVNGTAPKGAIAIEDSGE 336
DB 121 TLGNQMLLFNNSTTAGGAIYKKLELASSGLTLFRNSVNGTAPKGAIAIEDSGE 180
QY 337 LSLGADSGDIVFLGNVTSTTPGNNRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSST 396
DB 181 LSLGADSGDIVFLGNVTSTTPGNNRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSST 240
QY 397 TVTDVLKNETPADSALQYTGNIIPTEGKLSSETAADSKNLTSKLLQPVTLSCGTLSLKH 456
DB 241 TVTDVLKNETPADSALQYTGNIIPTEGKLSSETAADSKNLTSKLLQPVTLSCGTLSLKH 300
QY 457 GVTLOTQAFQOADSRLMDVGTLLPADTSTINNLVINISIDCAKAKIETKATSKNL 516
DB 301 GVTLOTQAFQOADSRLMDVGTLLPADTSTINNLVINISIDCAKAKIETKATSKNL 360
QY 517 TILSGTITLLDPTGTYFNHSLRNPSQYDILELKASGTVTSTAVTDPDPMGEKHFYGYQT 576
DB 361 TILSGTITLLDPTGTYFNHSLRNPSQYDILELKASGTVTSTAVTDPDPMGEKHFYGYQT 420
QY 577 WGPVWGTGASTATFNWTKGYINPERIGSLVNSLWNAFIDISSLHYLMETANEGLQ 636
DB 421 WGPVWGTGASTATFNWTKGYINPERIGSLVNSLWNAFIDISSLHYLMETANEGLQ 480
QY 637 GDRFWCAGLSNFFHKDSTKRRGRHLSSGGVIGGNLHTCSDKILSAFQCFDRDRY 696
DB 481 GDRFWCAGLSNFFHKDSTKRRGRHLSSGGVIGGNLHTCSDKILSAFQCFDRDRY 540
QY 697 FVAKNQGVYGGTLYQHNETYISLPCKLRPCSLSYVPEIPVLPSGNLSYTHTDNLKT 756
DB 541 FVAKNQGVYGGTLYQHNETYISLPCKLRPCSLSYVPEIPVLPSGNLSYTHTDNLKT 600
QY 757 KYTTPTVKSGWNSFALFEGGRAPICLDESALPEQYMPFMKLOFYVAHQGFKEQGTTE 816
DB 601 KYTTPTVKSGWNSFALFEGGRAPICLDESALPEQYMPFMKLOFYVAHQGFKEQGTTE 660
QY 817 AREFGSSRLVNLALPIGIRFDKESDCODATYMLTGYTVDLVRSNPDCTTILRISGDSWK 876
DB 661 AREFGSSRLVNLALPIGIRFDKESDCODATYMLTGYTVDLVRSNPDCTTILRISGDSWK 720
QY 877 TFGTNLARQALVLRAGNHCFNFSNFEAFQSFELRGSSRNYNVDLGAQYQF 928
DB 721 TFGTNLARQALVLRAGNHCFNFSNFEAFQSFELRGSSRNYNVDLGAQYQF 772

RESULT 2
Q823W9 PRELIMINARY; PRT; 926 AA.
AC Q823W9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polymorphic outer membrane protein G family
DE protein/autotransporter.
GN CCA00284.
OS Chlamydia caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83557;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carly H.A.,
RA Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoli P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydia caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae.";
RL Nucleic Acids Res. 31:2134-2147 (2003).
DR EMBL; AB016995; AAP05035.1; -.
DR TIGR; CCA00284; -.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia PMP.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF04415; Chlamydia_PMP; 1.
DR DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 5.
KW Complete proteome.
SQ SEQUENCE 926 AA; 98213 MW; 0E1062E0778658B2 CRC64;
Query Match 40.3%; Score 1923; DB 16; Length 926;
Best Local Similarity 43.2%; Pred. No. 3.8e-80;
Matches 412; Conservative 149; Mismatches 339; Indels 54; Gaps 17;
QY 1 MKSSPFKVFESTFAIFPLSM-----TATETVLDSSASFDGNKGNFSVRESQEDA 50
DB 1 MRPSLYKILISTLTIPLSFHSQVHAEVALTQESVLD-----NGAFSPQSTAG 52
QY 51 GTTYLFKGNVTLENIPTGTATITKSCPNNTKGLDFTTNGNSLLFQTVDAAGTVAGAAVNS 110
DB 53 GTTYNVESDISIVD-ACQAAAAMVSAAFVQTADLTFKNGRSLALENVNSGANPG-AIYV 110
QY 111 SVVDKSTTFIFGESSLPFASPCSSITTCGKAVSCSTGSLTKVNSLLFSKNFSTDNGA 170
DB 111 SAADKTLTLTDFSTLSPFKCPKHTVNTGKAVK-SGGALNLANNAASILFNQHSADGGA 169
QY 171 ITAKTLTLTGTTMSALFSENTSSKKGGAIGTSDALITITGNQGVFSNDTSSDGAIF 230
DB 170 ISCKAFSLTGSKSEISFTNTSTKKGGAIAATGVANLSDNQCKVIFSGNTAVNSGAVYA 229
QY 231 EASVTISNNAKVSFIDNKVTGASSTTGDMSGGAICAYKSTSTDKVTLTGNOMLLPSNT 290
DB 230 EANTTIAGNSAVVFNNAVTG-----TIDCGGAIHCSKTGATPVLTIRDNKVLFPKNT 284
QY 291 STTAGGAIYVKLELASGGLTLFSNSVNGTAPKGAIAIEDSGELSLSADSGDIVFLG 350
DB 285 SAAKGGAIYADKLYLTSGGPTVFGNKAT-NAAPKGAIGIAANGECSTIAEHGDTTFEN 343
QY 351 NTVTSTTPGT-NRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSSSTTVTVLKVNETPA 409
DB 344 NLIATANNATVKNAINIEGNGKFVNLRAASGNTLTFYDPIVVG--TAADLLTNQ--A 399
QY 410 DSALQYTGNIIFTGKLSSETAADSKNLTSKLLQPVTLSCGTLSLKHGVTLOTQAFQO 469
DB 400 EGTQVYNGRIIFSGEKLTEDQTADADNLKTVFTQPIALAAAGELILFNGVEVEKAVSQTA 459
QY 470 DSRLEMDVGTTLLE-PADTSTINNLVINISIDGAKAKIETKATSKNLTSKLLSGTITLLDPT 528
DB 460 GSLILIDAGTKLSAKTEDVTLTNLAINPNSLDGTKIATVAANNAKNTVTGAIGIIDPT 519
QY 529 GTFFYENHSLRNPSQYDILELKASGTVTSTAVTDPDPMGEKHFYGYQGTGPIVW----GT 584
DB 520 GKFYEDHKLNETLALGGIQFSKAGSITTTDVSTTTSPQAQHYGYQGNWS-LSWITDNGS 578
QY 585 GAST-TATFNWTKGYINPERIGSLVNSLWNAFIDISSLHYLMETANEGLQGRAPF 642
DB 579 DPKTQTAVFNWTKGYINPERIRAPILVNSLWSGSMFDIRSIQDVMSERSVDTLLETARGLW 638
QY 643 CAGLSNFFHKDSTKRRGRHLSSGGVIGGNLHTCSDKILSAFQCFGRDRDYFVAKNQ 702
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Db      639 VSGVGNELHDPKPSAENKFRHSISGYVLGATNTTSQEDTILSVAFQKQDKYLVAKNA 698
QY      703 GTVYGGTLYYQHNETYISL-----PCKLRPCSLSYVTEIPVLFSGNLSYTHNDLL 754
Db      699 ANVTAGSIYYQHVKSPDGLTRLENGPNTC-----CSGFSKEIPIFLDAQVYTYCHTNNM 752
QY      755 KTKYTYTPTVKSGWGNDSFALEFGGRAPICLDESALFEQYMPFMKLOFVVAHQGFKEQG 814
Db      753 TTTYTDYPEVKSGWGNDTVGVALSTSVPIPIFTHAFDVSAPPFAKLQVVAHQDFKEPT 812
QY      815 TEAREFGSSRLVNALPDIPIGRFKESQCDATYMLTGYVDLVRSPDCTTLIRISGDS 874
Db      813 REGRTFESSDLLNVSPVIGVKFKLVYGEKTAAYDLTLMYVDPVYRHNPCITGPAINDVT 872
QY      875 WKTFGTNLARQALVLRAGNHCFCNSFEAPFSQSFELRGSSRNVDLGAQYQF 928
Db      873 WLTTATNLARQAFIIRAGNHIAVTSGFEMPFSQGFELRSSRNVDLGAQVSP 926

RESULT 3
P71135 PRELIMINARY; PRT; 926 AA.
AC P71135;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative 98 kDa outer membrane protein.
OS Chlamydomophila abortus.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83555;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ovine abortion S26/3;
RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT "98kDa protein genes from ovine abortion strain S26/3 Chlamydia
RT psittacal.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72499; AAB18188.1; -.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF02415; Chlamydia_PMP; 2.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01376; POMP repeat; 6.
SQ SEQUENCE 926 AA; 98439 MW; 3E755E5F594750F CRC64;

Query Match 40.1%; Score 1915; DB 2; Length 926;
Best Local Similarity 42.9%; Pred. No. 8.8e-80;
Matches 410; Conservative 156; Mismatches 333; Indels 56; Gaps 18;

QY 1 MKSFFPKFVFSIFAIFLSM-----IATETVLDSASPDGKNGKNFVSRESQEDA 50
Db 1 MPRLYKILISLTLPISFHFSQLHAELVATQESILDA-----NGAFSPQSTAG 52

QY 51 GTTYLPGKVNLENIPGTGTAIKCFNNTKGDLTFTGNSNLLFTQVDAGTVAGAAVNS 110
Db 53 GTIYNVESDISVDV-GQTAAALASSAFVQTADNLTFKGNHLSLITNANAG-ANPAGINV 110

QY 111 SVVDKSTTFIGFSSLSFIASPGSSITGKAVSCSTGSLTKNVSLFSKFNSTDNGGA 170
Db 111 NTADKILTLTDPSKLSFKXCPSSLVNTGKAMK-SGGALNLANNASILPDQVYSAENGGA 169

QY 171 ITAKTILSLGTWMSALFSENTSSKKGCAQTSDALLITGNQGVFSVDNTSSDGAIAFT 230
Db 170 ISCKAFSLTGSSEKISFTTNTAKKGAAATAGIAHLSDNQGTIFRSGNTAVNSGAVYS 229

QY 231 EASVTISNNAKVSFIDNKVTKGASSITGDMGSGAICAYKTTSTDKVTLTGNCQMLLFSNNT 290
Db 230 EASMTIAGNNHVAFSNNVSGSS-----DCCGGAIHCSKTGSAPTIIRDNKVLFEENT 284

QY 291 STTAGGAIYVKLELASGGLTLFSRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLG 350

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Db      285 SSAAGGAIYTDKILTLTSGGPTAFINNKVTHAT-PKGAIGAANGECSLTRAHEGDIITFDN 343
QY      351 NTVTSTTPGT-NRSSIDLGTSAKMALRSAAGRAIYFYDPIITGSSSTTVTDVLKVNTEPA 409
Db      344 NLMATQDNATIKENAINIEGNGKFNVLRAASGKTSIFYDPIITVEGN--AADLLTLNKAEG 401
QY      410 DSALQYTGNIITFCEKLTSETEAADSKNLTSLKLOPVTLSGGLSLKKGVTILOQAFQTOA 469
Db      402 DKT--YNGRIIFSGEKLTEEQAAVADNLKTTFTQPIITLAAGELVLRSGVEAEKTVVQTA 459
QY      470 DSRLEMDVGTGLE-PADTSTINNVLINISSIDGAKAKIETKATSKNLTLSGTTLLDPT 528
Db      460 GSLILMDAGTKLSAKTEDATLTNLAINPNTLDGKFAVDVAAGKNVTLISGALGVIDPT 519
QY      529 GTIYENHSLRNPOSYDILELKASGTVTSTAVTDDPIMG-EKPHYGYQGTWGPVW----- 582
Db      520 GKFEYENHKLNDTLALGGIQLSGKGSVTTINV-PSHVVGVVAETHYGYQGNWS-VSWVKDNN 577
QY      583 GTCASTATATENWTGTGYIPNPERIGSLVPSNLWNAFIDISSLHYLMETANEG-LOGDRAF 641
Db      578 SDPKTOTAIPTWNTKGYVPNERRAPLVLNLSWGSFIDGESIQDVLERSVDSILETRGL 637
QY      642 WCAGLSNFFHKDKTKTRRFRHLSSGGYVIGGNLHTCSDKILSAAFCOLFCRDRDYFAKN 701
Db      638 WVSGIGNFFHKORNAENRKRHRHSSGVVLGATNTSREDSLSVAFCOLFAKDKDYLVSKN 697
QY      702 QGTVYGGTLYYQHNETYISL-----PCKLRPCSLSYVTEIPVLFSGNLSYTHDND 753
Db      698 AANVYAGSVYQHVSKFPDDLTRLFNPNTC-----CSGFSKEIPIFLDAQIYCHTANN 751
QY      754 LKTKYTYTPTVKSGWGNDSFALEFGGRAPICLDESALFEQYMPFMKLOFVVAHQGFKEQ 813
Db      752 MTSYTDYPEVKSGWGNDTLGLTSTSVPLPVPSSSIFDSYAPFAKLQVVAHQDDFKEP 811
QY      814 GTEAREFGSSRLVNALPDIPIGRFKESQCDATYMLTGYVDLVRSPDCTTLIRISGD 873
Db      812 TTIEGRVFESSDLLNVSPVIGIKFELKSYGERSAYDLTLMYIPDYRHNPCMTGLAINDV 871
QY      874 SWKTFGTNLARQALVLRAGNHCFCNSFNFAFSQSFELRGSSRNVDLGAQYQF 928
Db      872 SWLTATNLARQAFIIRAGNHIALTSQVEMFSQGFELRSSRNVDLGAQVAF 926

RESULT 4
Q823X1 PRELIMINARY; PRT; 942 AA.
AC Q823X1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polymorphic outer membrane protein G family protein/autotransporter,
DE putative.
DE CCA00282.
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RC MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzappple E., Khouri H., Federova M.B., Carty H.A.,
RA Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoi P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae.";
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AE016995; AAP05033.1; -.
DR TIGR; CCA00282; -.
DR InterPro; IPR003368; Chlamydia_PMP.

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QY 494 INISSIDGA---KKAKIETKATSKNLTSLGCTITLLDPTGTGYENHSLRNPOSY-DILELK 549
Db 419 INTASLGGGVPLAAQISABGTNKSVTIS-SLNLDVADGNGYEPYESTITREPFSLIEAK 477
QY 550 ASGTVTSTAVTPD-----PIMGEKPHYGQGTWGPVWGTGASTT---ATFNWTKTGYP 601
Db 478 ANGTGTPTPTTHLTDHAPAA-----HYGYQGLW-TTSWAQGTATTSQLATLAWQGTGYNP 532
QY 602 NPERIGSLVNSLWNAFIDISSLHYLMETANEGLQDRAFCWAGLSNPFHKDSTKTRGF 661
Db 533 NPERQGLPVENTLWGSFSDVRAIQNLMDISVNGADYQORGLWASGLANFLQKSGTETKRKF 592
QY 662 RHLSSGGYVIGNLTGSDTKILSAFAFCOLFGDRDIFYVAKNOGTVYGGTLYYQNETYISL 721
Db 593 RHHSAGYVLGAYAKTILSDVFSAAFCOLFGDRDKDYLKKNNSIYAGSIYQHTSFWDAW 652
QY 722 PCKLRPCSIYSVTEIPVIFSGNLSYTHDNDLTKYTT-----YPTVKGSGWGNDSF 773
Db 653 DNLLQ----STLGAQAPLVNAQLTYSHTSNDKTNMTTKYAPQGVVYPEIKGDWGNDCF 708
QY 774 ALFFGGRAPICLDESALFEQYMPFMKLQFYVAHOEGFKE-QGTEAREFGSSRLVNLALPI 832
Db 709 GVELGATVPIESPYSLFDMYSPLRQPLVYAHQEDFKENNSTEGRYFSSDLTNLSMPI 768
QY 833 GIRFDKESCDQATYNLTGTYVDLVRNPDCTTILRISGDS--WKTFTGNLARQALVLR 890
Db 769 GVKFERFSDNDIASYNVTLAYAPDLVRNPDCKTSLVSTYAVTLTKATNLARHAFIVK 828
QY 891 AGNHFCFNENFAFSPFSELRGSSRNYNVDLGAQYQF 928
Db 829 AGNYLSSSNFETFSQGFELRGSSRTYNVDLGSKIQF 866

RESULT 6
Q822Q5 PRELIMINARY; PRT; 841 AA.
AC Q822Q5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polymorphic outer membrane protein G family
DE protein/autotransporter.
GN CCA00624.
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
RA Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae."
RL Nucleic Acids Res. 31:2134-2147 (2003).
DR EMBL; AB016996; AAO05366.1; -.
DR TIGR; CCA00624; -.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; Chlamydia_PMP; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
KW Complete proteome.
SQ SEQUENCE 841 AA; 90411 MW; 21A9ED16E0D7C65D CRC64;

```

Query Match 34.9%; Score 1667; DB 16; Length 841;
 Best Local Similarity 40.7%; Pred. No. 1.7e-68;
 Matches 386; Conservative 127; Mismatches 278; Indels 158; Gaps 28;

```

QY 11 STFAIPPLSMIATETATYLDSSASPDGNKNGN-FSVRESQEDAGTTLFKGNVTLENIPGTG 69
Db 20 SFPA-----AAVOETLNSDSYNGNTTTPFPVKET--STGAETCNGNVCI-TVAGKT 70
QY 70 TAITKSCFNNTKGLDFTFTGNGNSLLFQTVDAGTVAGAAVNSSVVDKSTTTFIGFSSLSFIA 129
Db 71 TPLTKSCFTETTENLTFLOQGYSLCFDNITA-TAKPAAIEVSANDKTLISGISFLSFCSSY 129
QY 130 SPGSSITTKGAVSCSTGSLSLTKNVLSLLPSKNFSTDNGGAIKTAKTILSLTGTMTSALFSE 189
Db 130 CPFG--TTBQGAIQ-SKGVTTTFNNDKIIFENKCNSTKGGAIKCD-----TGT----- 174
QY 190 NTSSKKGGAIQTSALTITGNQGEVSFSDNTSSDGAIFTASVTISNNAKVPIDNKV 249
Db 175 -----NAEIKF----- 180
QY 250 TGASSSTTGMSGGAI CAYKTSITDTKVTLTGNQMLLFNNNTSTTAGGAIYVKKLELASGG 309
Db 181 -----EGNKYLLFSGNSSQOEGGAIYAKKLSIISGG 211
QY 310 LTLFSENSVNGTAPKGGAI AIEDS--GELSLSADSDGDIVFLGNTVTIST--TPGTRNSIDL 367
Db 212 PTLFNNSTSKAADPKGGAIC IADADSECLTAENGDIIFDGNKIITGTGTPSKRSIDL 271
QY 368 GTSAKMTALRSAAGRAIYFYDPIITGSSITVTDLKVNETPADSALQYTGNIIFTGEKLS 427
Db 272 GGGKFSQLRARDGFGVFPYDPIANGSD--TDTLEINK--ADGAATYSGRIVFSEKLT 327
QY 428 ETEAADSKNLTSLKLPVTLSGGTLSLKHGVTLQTOAFTQADSRLEMDVGTTLLEPADTS 487
Db 328 EDEKQVTDNLKGFQKPLTVGSGSFVLKNGVTVSAAQITQSGGA-IEMDAGTNL----IS 382
QY 488 T-----INNLVINISSIDA---KKAKIETKATSKNLTLSGTTITLLDPTGTGYENHSLRN 539
Db 383 TTEDISLNLVINTASLGGGVPLAAQISABGTNKSVTIS-SLNLDVADGNGYEPYFVST 441
QY 540 POSY-DILELKASGTVTSTAVTPD-----PIMGEKPHYGQGTWGPVWGTGASTT---A 590
Db 442 TREFPSSIEAKANGTGTPTPTTHLTDHAPAA-----HYGYQGLW-TTSWAQGTATTSQLA 496
QY 591 TFNWTKTGYPNPERIGSLVNSLWNAFIDISSLHYLMETANEGLQDRAFCWAGLSNFF 650
Db 497 TLAWOQTGYNPNERQGPLVPNTLWGSFSDVRAIQNLMDISVNGADYQORGLWASGLANFL 556
QY 651 HKDSTKTRGFRHLSGGYVIGNLTGCTSKILSAARCOLFGDRDIFYVAKNOGTVYGGTL 710
Db 557 QKSGTETKFRHRSAGYVLGAYAKTILSDVFSAAFCOLFGDRDKDYLKKNNSIYAGSI 616
QY 711 YIQHNETYISLPCLRPCSLSVYVTEIPVLFSGNLSYTHDNDLTKYTT-----YP 762
Db 617 YIQHTSFWDADNLLQ----STLGAQAPLVNAQLTYSHTSNDKTNMTTKYAPQGVVYP 672
QY 763 TVKSGWGNDSFALFEGGRAPICIDESALFEQYMPFMKLQFYVAHOEGFKE-QGTEAREFG 821
Db 673 EIKGDWGNDCFGVELGATVPIESPYSLFDMYSPLRQPLVYAHQEDFKENNSTEGRYPE 732
QY 822 SSSLVNLALPIGIRPKESDCQDAYNLTYVDLVRNPDCTTILRISGDS--WKTFTG 879
Db 733 SSDLTNLSMPIGVKFERFSDNDIASYNVTLAYAPDLVRNPDCKTSLVSTYAVTLTKA 792
QY 880 TNLARQALVLRAGNHFCFNENFAFSPFSELRGSSRNYNVDLGAQYQF 928
Db 793 TNLARHAFIVKAGNYLSLNSNFEIFSQGFELRGSSRTYNVDLGSKIQF 841

RESULT 7
P77792 PRELIMINARY; PRT; 839 AA.
ID P77792;
AC P77792;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE POMP90B precursor.

```



```
QY 177 SLGTTMSALLFSENSSKKGAIQTSDALITIGNQGEVFSFSDNTSSDGAIFTEASVTI 236
Db 178 S-----SEAEIKI 185
QY 237 SNNAKVSFIDNKVTGASSSTTGDMSGGAI CAYKTSTDTKVTLTGNOMLLFSNNVTSTAGG 296
Db 186 EN-----NQNLVFAENSSSSGG 203
QY 297 AIYVKLELASGGITLFSRNSVNGGTAPKGAIAIEDS-GRLSLSADSQDIFVFGNVTIS 355
Db 204 AIYADKLITVSGGPTLFSNNVS-ASSPKGGAICIKUSGGECSTALDGDITFCNKIKI 262
QY 356 T---TPGTRSSIDLGTSAKWTALRSAGRAIYFDPITTTGSSSTTVTLVKWNETPADSA 412
Db 263 TNGGSPVTTRNSIDLGSQKFTKLNAKEGFGIFDYDITGGG-----DELNINK--QDT 315
QY 413 LQYTGNIIFGEKLESETEADSKNLTKLLOPVTLSGGTSLKHGVTLOQAFQOQADSR 472
Db 316 VDTYTKLVFSGERLUSDEKKVAANKLSDPKQLKIGSGSLILDKGVTLTKSFQTQEGAT 375
QY 473 LEMDVGTTLBP-----ADTSTINNLVINISSIDGA---KKAKIETKATSKNLTSGTITL 524
Db 376 VMVDLGTTLQTPSSGGTITLNLNDINVASLGGGVADPKVEATTESKTVIIN-AVNL 434
QY 525 LDPTGFYENHSLRNPOSYDILELK--ASGTVTSTAV-----TPDPIMGKPFHYGQGTW 577
Db 435 VDDGNAYEYFILAASQPFATAIEVRSGSGSITKPTTNLENYTPPT-----HYGYQGNW 488
QY 578 GPIVWVGTAET---TATFNMTKCYIENPERIGSLVPSNLWNAFIDISLHYLMETANEG 634
Db 489 -TWTWKQSSAQEKATATLTWEQGYSPNPERQSGSLVENTLWGSFSDIRATQNLMDISVNG 547
QY 635 LOGDRAPWCAGLGNFFHKDKSTKRRGRPHLSGGVIGGNLHTGSDKILSAAPCOLFGRDR 694
Db 548 ADVHRGFWSVGLGNFLHKSQSDTKRKRHNSAGVALGVYAQTSEDVFSAPCOLFGKDK 607
QY 695 DYFVAKNQGVYGGTYLYQHNETYISLPCKRLPCSLSYVPT-----EIPVLFSG 743
Db 608 DYLVSKNSSTVYAGSIYYQH-----ISYWNNTWNTLLQNTLGAEPVLNA 652
QY 744 NLSYTHDNDLTKY-----TTPYTKVSGWNSDFALEFGGRAPICLDSEALPEQYM 795
Db 653 QLAYCHASNMTKMTMDTYAPPKTTSYSEIKGDWGNDFGVEFGAKAPI-ETASILLFDMYS 711
QY 796 PFMKLOFVYAHQGFKEQGT-EAREFGSSRLVNLALPIGIRFDEKSDQCATVNLTLGYT 854
Db 712 PFVKLQLVHAHQDDFKENNSDQGYFESNNLTNLSMPIGVKLEKFSHKDTASNLTILAYA 771
QY 855 VDLVRNPDCITLIRISGDS--WKTFTGNLARQALVLRAGNHFCFNSNFEAFSQSFELR 912
Db 772 PDIVRSNPDCATSLVSPTSVAVWTKANNLARHAFILQAGNYLALTRNTLFSQGFELR 831
QY 913 GGSRRNVNVLGAKYQF 928
Db 832 GSCRTNIDLGSKIQF 847
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RESULT 9

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P71133
ID P71133 PRELIMINARY; PRT; 846 AA.
AC P71133;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE POM91B precursor.
OS Chlamydia abortus.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OC NCBI_TaxID=83555;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=S26/3;
RX MEDLINE=96406378; PubMed=8810511;
RA Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;
```

Identification of a multigene family coding for the 90 kDa proteins of the ovine abortion subtype of Chlamydia psittaci.;
FEMS Microbiol. Lett. 142:277-281(1996).
[2]

SEQUENCE FROM N.A.

```
RC STRAIN=S26/3;
RX MEDLINE=98187897; PubMed=9529048;
RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT "Molecular cloning and characterization of the genes coding for the highly immunogenic cluster of 90-kilodalton envelope proteins from the Chlamydia psittaci subtype that causes abortion in sheep.";  
RL Infect. Immun. 66:1317-1324(1998).  
DR EMBL; U65943; AAC15923.1; -;  
DR InterPro; IPR003368; Chlamydia PMP.  
DR Pfam; PF02415; Chlamydia PMP; I.  
DR TIGRFAMs; TIGR01376; POMP_repeat; 3.  
KW Signal.  
FT SIGNAL  
FT CHAIN  
SQ SEQUENCE 846 AA; 90834 MW; 4CDC31DC03C2964E CRC64;
```

Query Match 33.6%; Score 1604.5; DB 2; Length 846;
Best Local Similarity 38.7%; Pred. No. 1.3e-65;

Matches 368; Conservative 140; Mismatches 269; Indels 173; Gaps 26;

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QY 23 TETVLDSSASFDGN-KNGNFSVRESQEDAGTYYLFGKNTVLENIPTGTALTYSFNTK 81
Db 26 TNEITLSSSYNGNVTISDEFVKET---TSGAIVTCGNVCI-SYAGKDSPLNKSCEFST 82
QY 82 GDLTFTGNGNSLLFQTVADGTAGAAVNSVDKSTTFIGFS--SLSFASPGSSITGK 139
Db 83 ENLSFIIGNGYTLCFDNIITQSSHPGALSVDGNTKLDISGSLFSCAYCCPPG---TTGY 139
QY 140 GAVSCSTGSLSTKYNVSLLFKSNFSTNDGAIYAKTSLTGTMTMSALFSENTSKKGAI 199
Db 140 GAIQ-TKGTTLTKDNGSLVFHKNCSTAEAGAIQCK----- 173
QY 200 QTSDALITIGNQGEVFSFSDNTSSDGAIFTEASVTSNNAKVSFIDNKVTGASSSTTGD 259
Db 174 -----SSSSTAE 180
QY 260 MSGGAI CAYKTSTDTKVTLTGNOMLLFSNNVTSTAGGAIYVKKLELASGGLTLFSRNSVN 319
Db 181 LK-----LENNKNLVFSENSSKEKGAIYADKLTVSGGPTLFSNNVS 224
QY 320 GGTAPKGAIAIEDS-GRLSLSADSQDIFVFGNVTST---TPGTRSSIDLGTSAKMTA 375
Db 225 HNSSPKGAICIKDSQDREGSLTANLGDITFDGNKIITTINGGSPVTTRNSIDLGSQKFTK 284
QY 376 LRSAAGRAIYFVDPI-TTGSSTTVTLVKWNETPADSAQYTCGNIITFGEKLESEEAADS 434
Db 285 LNAKEGFGIFDYDPIANTGGSTEI-----ELNKTESDTT--YTKIVFSGEKLSDSEKTVP 338
QY 435 KNLTSKLLQFVTLISGGTSLKHGVTLTQOAFQOQADSRLEMDVGTTL-----PADTSTIN 490
Db 339 ANLKSIFYKQPLKTAGSLVKDGVTLAKKIQTQKSTVMDLGTTLQTPSSSGEITLT 398
QY 491 NLVINISSI---DGAKKAKIETKATSKNLTSGTITLTDPTGTFYENHSLRNPOSYDILE 547
Db 399 NLDIINIASLGGGGGTAPAKLATATNASQAISIA-AVNLVNTDSNTYEDPILSASKSPSAI- 456
QY 548 LKASGTVTSTAVTTPDPIMGKEF-----HYGYQGTWGPVWGTGAST---TATFNWTKTYI 600
Db 457 ---TATSSSTVTPPETNLUKNYTPPTHYGYQGNW-TVTWKQSSAQEKATATLTWEQGY 512
QY 601 PNPERIGSLVPSNLWNAFIDISLHYLMETANEGLQGDRAFWCAGLSNFFHKDKSTKRRG 660
Db 513 PNPERVGSILVPTNLGAFSDTTRAIQNLMDISVNGADYSGRFPWVSSLANFLNKSQDTEK 572
QY 661 FRLHSGGVYIGNLHNTCSKILSAAPCOLFGRDRDYFVAKNQGVYGGTYLYQHNETYIS 720
Db 573 FRHHSAGYALGVYAQTSPSDVCSAAFCQLFGKDKDYFVSKNSSTIYAGSIYYQH----- 626
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Qy 721 LPCKLRPCSLSYVPT-----EIPVLFSGNLSYTHDNDLTKYK-----TY 761
Db 627 -----ISYWNWTNLLQNTLGAEPVLNAQLTYCHASNKNKTNMTNITTPKNTVP 677
Qy 762 PTVKSGWNSDFALEFGGRAPICLDESALFQYMPFMKLOFYAHQEGFKEQGT-EAREF 820
Db 678 SEIKGDWNSDCEGVEFGAKAPI-ETASLLFDMYSFVKQLQVHAHQDDFKNNSDQGRYF 736
Qy 821 GSSRLNLALPIGRFDRKESDQATYNTLGYTVDLVRSPDCTTTILRISGDS--WKTF 878
Db 737 ESNLNLNLSMPLGVKLEFESHKDTASYNTLAYAPDIVRSPDCTASLLVPTSVAWVTK 796
Qy 879 GTNLARQALVLRAGNHCFNSNFAPSFQSFELRGSSRNYNVDLGAQYQF 928
Db 797 ANNLAHAFILQAGNYLALTRNTELFQFELRGSCRTYNIDLGIQF 846

RESULT 10
Q823X5
ID Q823X5 PRELIMINARY; PRT; 1011 AA.
AC Q823X5;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Polymorphic outer membrane protein G family
DE protein/autotransporter.
GN CCA00278.
OS Chlamydophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzapflee E., Khouri H., Federova N.B., Carty H.A.,
RA Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoi P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae."
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AB016995; AAP05029.1; -.
DR TIGR; CCA00278; -.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF02415; Chlamydia_PMP; 1.
DR TIGRFAMS; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMS; TIGR01376; POMP_repeat; 6.
KW Complete proteome.
SQ SEQUENCE 1011 AA; 107952 MW; EBDAGFAIC46EDEB6 CRC64;

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Query Match 29.5%; Score 1410.5; DB 16; Length 1011;
Best Local Similarity 34.4%; Pred. No. 1.2e-56;
Matches 360; Conservative 157; Mismatches 377; Indels 151; Gaps 30;

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```

Qy 1 MKSSFPKVFESFPAIFPLSMIA-TEVLDSSAFDGNKNGNSVRSEQEDAGTTLFKGN 59
Db 1 MKASLAKFLISTLTLLPYFQAFSLVVPNGYDGNLRETFFYTITSNPEGTTALSGN 60
Qy 60 VTLENIPTGTALTATKSCFNNTKGDLTFTGNGNLLPQTVDAGTVAGAAVNSVVDKST-- 117
Db 61 LNLNLNLSNVAIPSCFFNSAGSMITVGRNHLTF--TNLRTSANGAALSIPPTTPES 118
Qy 118 ----TFTGFSLSF-----IASPGSITTG-KGAVSCSTGSLTKNWSLLSKNF 163
Db 119 FPTYIKGVNLTSPSNCLALMARTTTPNTTPVNPNGAFYKAPVLENIQNVLPKNNR 178
Qy 164 STD-----NGGAITA-KTSLTGTMTSALPSENTSSKK 195

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Db 179 AADSGGLWVETAGISNLIKSMQFLSNVGANGAINASKSLDVT-QCPISILFRSNSAEKL 237
Qy 196 GGAITQSDALFITGNOGEVSFDNMS-----SDSGAAITFEASVTISNNAKVSFIQNK 248
Db 238 GGAIOAVDPATTNQVNTAVRESENGSVQFDANNAKSGGAIYSKGNVDFSNNAQL-LIQNN 296
Qy 249 VTGASSSTTGM--SGGAI-CAYKTSID-----TKVTLTGOMLLFNSNTST 292
Db 297 SASPEVANTNEVLGGGGAIFCVOQTPTQPPPPPTTNPVFSGLTITNQKILLPANFAA 356
Qy 293 TAGGAIYVKLELASGGTLTFRSNVNGGTAPKGAIAIEDSGELSLSDSGDIYVFLGN- 351
Db 357 TAGGAIYGEKYSITSSGKMTFTN-----IAKGGAIYIPENGELTISADYGDIMFYENL 411
Qy 352 -----TVTSTPGNRRSIDIGTSAKMTALSAAGRAIYFYDPITT-----GSSTTVDVLK 403
Db 412 KKDDATVT-----RNAVTLAKGATIKLLAASGDHKLCFYDPIVTTLPETAPTNDKTLT 464
Qy 404 VNETPADSA--LOYTGNIIPTGEKISETEAADSKNLTSLKLPQVTLTSGTISLKHGVTIQ 461
Db 465 INQDKTSTPTPTNYITGLLFGAYVDSQSASTANFESTIYQKVLGGKVLADKASLS 524
Qy 462 TOAFTQADSRLEMDVGTTL-----EPADTS---TINNVLIN 495
Db 525 VASFTQETDSILLMDNGTTLAITEHSHQTPAAGGGGGGGTPTQEAANTDGVISLNLHVN 584
Qy 496 ISSI-DGAKKAKIETKATSKNLTLSGTTLLDPTGTFYENHSLRNPQ--SYDILELKASG 552
Db 585 ISSITEQEGAKLETNTDGTITLTHVSLDDVSGTAYENHDLFNKDTVTINLLSLSTAG 644
Qy 553 TVTSTAVTPD-PMIGE-KFHYGYQGTGPIVWGTGASTT-----ATFNWTKTGPINPE 604
Db 645 DSKTTINGLDTLRGDABPQYQGSW-QLAWENGADANKQKILKAT--WTKTGTPTNPE 701
Qy 605 RIGSLVPSNLNAPIDISSIHYLMETANEGLQDRAFCAGLSNPFPHKDSKTKRGRFHL 664
Db 702 ROASLVPSNLGAFIDLSRMAALATASCDGFGYKGLWAGISNIFPHDRNSVSHGFRI 761
Qy 665 SGYVIGNLTCSDKILSAFCQLFGRDRDYFAKNQGTVVGTTLYOHNETHYISLPCK 724
Db 762 SGYVIGANSQTVDTSVFGVAFSQIFAKSKDYVSVSSAKSAQIAGS-----AYLSVKQ 814
Qy 725 LRPCSLSYVPTETIPVLFSGNLSYTHDNDLTKYKTYPTVKGSGWNSDFALEFGGRAPIC 784
Db 815 LSNITFS-----SFAIRINISHTNEDMKRTYTFIPEKDNWNNCWLGEIGSLPIV 866
Qy 785 LDESAL-FEQYMPFMKLOFYAHQEGFKEQGTAREFGSSRLVNLALPIGIRFDKESDQ 843
Db 867 LQITKLHLNLIIPFNNVQLGYAEHGSFKELAEARSFCSRLINLAVPVGFKIDRRSHS 926
Qy 844 DATYNLTGYTVDLVRSPDCTTTILRISGDSWKTGTGNLARQALVLRAGNHCFNSNFA 903
Db 927 PDFYSLAISYIPDVVWRNPGCNTLLANGVRWKTPTATNLNRHGLMQGSHTHAVLSNIEI 986
Qy 904 FSQSFELRGSSRNYNVDLGAQYQF 928
Db 987 FSHGSCELRSSRNYNVNGSKIRF 1011

RESULT 11
Q8VU49
ID Q8VU49 PRELIMINARY; PRT; 602 AA.
AC Q8VU49;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Putative polymorphic membrane protein (Fragment).
OS Chlamydia psittaci (Chlamydophila psittaci).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83554;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=LLG;

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QY 377 RSAAGRAIYFDPI--TTGSSSTTVTDVLKVNETPADSALQYTGNIIFTGEKLSETEADSK 435
DB 283 NAKEGGFIHFDPIANTGSTEI-----ELNKTESDIT--YTGIKIVSGEKLSDEEKTVPD 336
QY 436 NLTSKLLQPVTLSSGGTSLSKHGHTLTQTOAFTQOADSRLMDVGTILE----PADTSTINN 491
DB 337 NLKSYFKQPLKIGAGSLVLKDGVTLEAKKITQKSTVVMVMDLGTTLQTPSSSGETITLTN 396
QY 492 LVINISSI---DQAKAKIETKATSKNLTLSGITITLLDPTGTFYENHSLRNPOSYDILEL 548
DB 397 LDINIASLGGGGGTAPAKLATNTASQAISTA-AVNLVNTDSNTYEDPILSASKSFSAI-- 453
QY 549 KASGTVTSTAVTDPDPMGEKF----HYGYOGTWGPIVWGTGAS---TTATFNWTKTGYP 601
DB 454 --TATTSSSTVTPETNLKNYTPPTHYGYQGNW-TLAWPGETWQLKATLWNEQTYGSP 510
QY 602 NPERIGSLVNSLWNAFIDISSUHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKRRGF 661
DB 511 NPERVGSVPLTLWGSFSDIRAIQNLMDSVNGADYSRGFWVSGLANFLNKSNGTHKRF 570
QY 662 RHLSGGYVIGGNLHTCSDKILSAAPCOLFGRDRDYFAKKNQGTGYGGTLYYQHNETYISL 721
DB 571 RHNSAGYALGVYAQTPESEDIFSAAPCOLFGKDKDYFLSKNSSTIYAGSIYYQH----- 623
QY 722 PCKLRPCSLSY-----VPTIPLVFLSGNLSYTHTDNDLTKYT-----TYP 762
DB 624 -----ISYWNWQNLLQNTTGAEPVLVNAQLTYCHASNMMKNTMTNTYTPKNVTPS 675
QY 763 TVKSGWGNDSFALEFGGRAPI 783
DB 676 EIKGDWGSDFGVFEFGAKAPI 696

RESULT 15
Q8VU48 PRELIMINARY; PRT; 581 AA.
AC Q8VU48;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Putative polymorphic membrane protein (Fragment).
OS Chlamydia psittaci (Chlamydia phila psittaci).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phila.
OX NCBI_TaxID=83554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=POS;
RA Laroucau K., Souriau A., Rodolakis A.;
RT "Isolation of a new pmp sequence and evidence of pmp polymorphism in
RT serotype-1 Chlamydia psittaci strains.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243419; AAL36963.1; -.
DR InterPro; IPR003369; Chlamydia_PMP.
DR Pfam; PF02415; Chlamydia_PMP; 1.
FT NON TER 1
SQ SEQUENCE 581 AA; 62860 MW; CDDF3C98522E112F CRC64;

Query Match 24.6%; Score 1172.5; DB 2; Length 581;
Best Local Similarity 40.4%; Pred. No. 4.7e-46;
Matches 253; Conservative 100; Mismatches 185; Indels 89; Gaps 17;

QY 344 GDIVFLGNTVSTTPGN---RSSIDLTSAKMTALBSAAGRAIYFYDPI--TTGSSSTTVT 399
DB 2 GDITFDGNKLIITRSSTTVKRNISISLGGGKFTKLNKAGEGFIFFYDPIANTGDTNTEI 61
QY 400 DVLKVNETPADSALQYTGNIIFTGEKLSETEADSKNLTSLKLPVTLSSGGLSLKHGVT 459
DB 62 ELNKAEE---GGSTTYTGKIVSGEKLSDEBKVADNLKSYFTQPLKIGAGSLVLKDGVT 117
QY 460 LQTAFTQOADSRLMDVGTTLBPA----DTSTINNLVINISSIDGA----KKAKIETKAT 512
DB 118 LEAKKVSQTDGSTAVMDLGTTLQTSSTSGETITLTNLDINVASLGGGGVAPDPAKVEAQA 177
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```
QY 513 SKNLTLSGITLLDPTGTFYENHSLRNPOSYDILELKASGTVTSTAVTPD-----PIMG 566
DB 178 GKTVITIN-AVNLVDTDGNAYEPILATSQFTAILIAKAGSSGTTTTPTDNLKNYTPPT-- 234
QY 567 EKPHYGYOGTWGPIVWGTGAST---TATFNWTKTGYPNPERIGSLVNSLWNAFIDISS 623
DB 235 ---HYGYQGNW-TVTKLGTSAQEETATLWNEQTYGSPNPERVGSVLPNLTWGSFSDIRA 290
QY 624 LHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRGRFHLSCGYVIGGNLHTCSDKILS 683
DB 291 IQNLMDSVNGADYSRGFWVSGLANFLNKSNGTHKRFHNSAGYALGVYAQTPESEDIFS 350
QY 684 AAFCOLFGRDRDYFAKKNQGTGYGGTLYYQHNETYISLPCLRPCSLSY----- 732
DB 351 AAFCOLFGKDKDYFLSKNSSTIYAGSIYYQH-----ISYWNWQNLLQNT 395
QY 733 VPTIPLVFLSGNLSYTHTDNDLTKYT-----TYPTVKGWGNDSFALEFGGRAPIC 784
DB 396 IGAEAPLVNLNAQLTYCHASNMMKNTMTNTYTPKNVTPSEIKGDWGSDFGVFEFGAKAPI- 454
QY 785 LDESALFEQYMPMKLOFYVAHQEGEKEQGT-EAREFGSSRLVNLALPIGIRFDKESDCQ 843
DB 455 ETASLLFDMYSPEVKLQLVHAHQDDFKENSDQGRYFESNNLTNLSMPTIGVKLEKFSHED 514
QY 844 DATYNLTGLGYTVDLVRSNPDCTTTLRAISGDS--WKTFTGNLRAQALVLRAGNHFCFNSNF 901
DB 515 TASNLTILAYAPDIVRSNPDCTASLLVSPTSVAVWVTKANLARHAFILQAGNYLA----- 569
QY 902 EAFSQSFELRGSSRNINVDLGAKYQF 928
DB 570 -----TYNIDLGSKIQF 581
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Search completed: August 10, 2004, 13:14:18
Job time : 50 secs

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 13:00:44 ; Search time 774 seconds
(without alignments)
16465.884 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 3000

Sequence: 1 cgccttactagtagaggT.....tggttgctaaacactttc 3000

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3000	100.0	3000	3	AAA27021 Chlamydia
2	2975.4	99.2	110000	2	AAX31990_00 Nucleotid
3	2775.6	92.5	2787	2	AAX06820 Chlamydia
4	2241	74.7	2241	6	ABL91193 Chlamydia
5	546.6	18.2	2781	6	ABQ84775 Chlamydia
6	546.6	18.2	2781	6	ABQ78033 Chlamydia
7	546.6	18.2	2781	7	ABX99200 C. psitta
8	531.2	17.7	273254	3	AAC81914 Chlamydia
9	530.2	17.7	2815	2	AAX06817 Chlamydia
10	527	17.6	2787	6	ABL91231 Chlamydia
11	524.6	17.5	2957	3	AAX61509 DNA encod
12	523	17.4	534	6	ABL91192 Chlamydia
13	522.2	17.4	2757	2	AAX06821 Chlamydia
14	518.4	17.3	110000	2	AAX31990_05 Continuation (6 of
15	518.2	17.3	2950	3	AAA30851 Chlamydia
16	516.6	17.2	2787	6	ABL91200 Chlamydia
17	516.6	17.2	273254	3	AAC81914 Chlamydia
18	515.2	17.2	2784	3	AAA30852 Chlamydia
19	515	17.2	2787	2	AAX06822 Chlamydia
20	514	17.1	2793	2	AAX06823 Chlamydia
21	514	17.1	2793	6	ABL91206 Chlamydia
22	514	17.1	2793	7	ACA30626 Prokaryot
23	513.6	17.1	3000	3	AAA30853 Chlamydia

24	512.6	17.1	2950	3	AAA30849	Aaa30849 Chlamydia
25	509.8	17.0	110000	2	AAX31990_05	Continuation (6 of
26	506.6	16.9	3050	3	AAA48838	Aaa48838 Chlamydia
27	506	16.9	3000	2	AAX06828	Aax06828 Chlamydia
28	503.6	16.8	2811	6	ABL91260	Ab191260 Chlamydia
29	503.6	16.8	2811	7	ACA30625	Aca30625 Prokaryot
30	496.2	16.5	110000	2	AAX31990_04	Continuation (5 of
31	491.8	16.4	2790	3	AAA30854	Aaa30854 Chlamydia
32	477	15.9	2808	3	AAA48839	Aaa48839 Chlamydia
33	469.4	15.6	2784	3	AAA30850	Aaa30850 Chlamydia
34	465.8	15.5	2787	6	ABL91241	Ab191241 Chlamydia
35	465.8	15.5	2787	7	ACA30627	Aca30627 Prokaryot
36	465.8	15.5	2950	3	AAA30847	Aaa30847 Chlamydia
37	465.8	15.5	3200	2	AAX06816	Aax06816 Chlamydia
38	435.8	14.5	2784	3	AAA30848	Aaa30848 Chlamydia
39	389	13.0	3050	3	AAZ61508	Aaz61508 DNA encod
40	378.4	12.6	2838	2	AAX06827	Aax06827 Chlamydia
41	348.8	11.6	2750	3	AAA28690	Aaa28690 C. pneumo
42	348.4	11.6	2520	6	ABQ84758	Abq84758 Chlamydia
43	348.4	11.6	2520	6	ABQ78016	Abq78016 Chlamydia
44	348.4	11.6	2520	7	ABX99183	Abx99183 C. psitta
45	345	11.5	2526	3	AAA28691	Aaa28691 C. pneumo

ALIGNMENTS

RESULT 1
AAA27021
ID AAA27021 standard; DNA; 3000 BP.
XX
AC AAA27021;
XX
DT 15-SEP-2003 (revised)
DT 11-AUG-2000 (first entry)
XX
DE Chlamydia pneumoniae 98kD putative outer membrane protein gene.
XX
KW Chlamydia; antigen; vaccine; infection; outer membrane protein; ds.
XX
OS Chlamydia pneumoniae.
FH Key Location/Qualifiers
FT CDS 101..2887
FT /*tag= a
FT /product= "98kDa putative outer membrane protein"
XX
WO2000026237-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-GB003579.
XX
PR 29-OCT-1998; 98US-0106070P.
PR 01-MAR-1999; 99US-0122066P.
PR 27-OCT-1999; 99US-00428122.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Murdin AD, Oomen RP, Dunn PL;
XX
WI: 2000-365569/31.
XX
P-PSDB; AAY94327.
XX
PT Novel Chlamydia 98 kDa putative outer membrane protein antigen, used for
XX
PS vaccination and protection against Chlamydia infection.
XX
PS Claim 1; Fig 1; 93pp; English.
XX
CC The present sequence is the 98kDa putative outer membrane protein gene
XX
CC from Chlamydia pneumoniae. The genomic sequence was amplified using two
XX
CC PCR primers. The 5' primer contains a NotI restriction site, a ribosome
XX
CC binding site, an initiation codon and a sequence close to the 5' end of

cc the 98kDa putative outer membrane protein coding sequence. The 3' primer
cc contains the sequence encoding the C-terminal sequence of the putative
cc outer membrane protein and a Bergi restriction site. The stop codon was
cc excluded and an additional nucleotide was inserted to obtain an in-frame
cc C-terminal fusion with the Histidine tag. The PCR product was cloned into
cc a eukaryotic expression vector (pCA-Myc-His) by restricting both the
cc vector and the PCR product with NotI and BamHI and performing a ligation
cc reaction. This expression vector was injected intramuscularly and
cc intranasally into mice, which were subsequently inoculated with Chlamydia
cc pneumoniae. The chlamydial lung titers of the immunised mice were lower
cc than those of the controls. Thus the 98kDa putative outer membrane
cc protein can be used as a vaccine to provide protection against Chlamydia
cc infections, especially Chlamydia pneumoniae infections. The polypeptide
cc may also be administered orally to treat Chlamydia infection. The present
cc sequence may also be used in the construction of attenuated Chlamydia
cc strains that can over-express the gene or express it in a non-toxic form.
cc (Updated on 15-SEP-2003 to standardise OS field)

xx SQ Sequence 3000 BP; 871 A; 617 C; 634 G; 878 T; 0 U; 0 Other;

Query Match	100.0%;	Score 3000;	DB 3;	Length 3000;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3000;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	CGCTCTTACCTAGTAGAGTTGACGTGAATTTCTTGACTTGTTCTCCTATTTGGTGTACT	60		
Db 1	CGCTCTTACCTAGTAGAGTTGACGTGAATTTCTTGACTTGTTCTCCTATTTGGTGTACT	60		
QY 61	CTTAAATATTAATTAATCAAAATCAAAATATATTTTCAATGAAGTCTTTTCCCCAA	120		
Db 61	CTTAAATATTAATTAATCAAAATCAAAATATATTTTCAATGAAGTCTTTTCCCCAA	120		
QY 121	GTTCGTATTTTACATTTTGTCTATTTTCCCTTTGTCTATGATGCTACGACAGATTTT	180		
Db 121	GTTCGTATTTTACATTTTGTCTATTTTCCCTTTGTCTATGATGCTACGACAGATTTT	180		
QY 181	GGATTCAAGTGGAGTTTCGATGGGAATATAATGTAATGTTTTCAGTTCGTGAGAGTCA	240		
Db 181	GGATTCAAGTGGAGTTTCGATGGGAATATAATGTAATGTTTTCAGTTCGTGAGAGTCA	240		
QY 241	GGAAGATGCTGGATCTTCTATTTGTTTAAAGGGAATGTCATCTAGAAATATTTCTGG	300		
Db 241	GGAAGATGCTGGATCTTCTATTTGTTTAAAGGGAATGTCATCTAGAAATATTTCTGG	300		
QY 301	AACAGGCAAGCAATACAAAAAGCTGTTTAAACACACTAAGGCGATTTCACTTTAC	360		
Db 301	AACAGGCAAGCAATACAAAAAGCTGTTTAAACACACTAAGGCGATTTCACTTTAC	360		
QY 361	AGGTAACGGGAATCTCTATTTGTTTCCAAACGGTGGATGCGAGGACTGTAGCGGGCTGC	420		
Db 361	AGGTAACGGGAATCTCTATTTGTTTCCAAACGGTGGATGCGAGGACTGTAGCGGGCTGC	420		
QY 421	TGTTAACACAGCGTGGTAGATAAATCTACACAGTTTATAGGGTTTCTTCGTATCTTT	480		
Db 421	TGTTAACACAGCGTGGTAGATAAATCTACACAGTTTATAGGGTTTCTTCGTATCTTT	480		
QY 481	TATTCGGTCTCTGGAAGTTGATTAACCTACCGGCAAGAGCGGTGTGCTCTACGGG	540		
Db 481	TATTCGGTCTCTGGAAGTTGATTAACCTACCGGCAAGAGCGGTGTGCTCTACGGG	540		
QY 541	TAGCTTGAGTTTGACAAAAAATGTCAGTTTGTCTTTTCAAGAAAACTTTTCAACGGATAA	600		
Db 541	TAGCTTGAGTTTGACAAAAAATGTCAGTTTGTCTTTTCAAGAAAACTTTTCAACGGATAA	600		
QY 601	TGGCGGTGTATCACCGCAAAACTCTTTCAATTAACAGGGAATCAATGTCTGCTGTT	660		
Db 601	TGGCGGTGTATCACCGCAAAACTCTTTCAATTAACAGGGAATCAATGTCTGCTGTT	660		
QY 661	TTCTGAAATACCTCTCTCAAGAAAGCGGAGCCATTACAGCTTCGATGCCCTTACCAAT	720		
Db 661	TTCTGAAATACCTCTCTCAAGAAAGCGGAGCCATTACAGCTTCGATGCCCTTACCAAT	720		
QY 721	TACTGGAAACCAAGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGC	780		

Db 721	TACTGGAAACCAAGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGAATCTGGAGCTGC	780
QY 781	AATTTTACAGAAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCTTTATTGACAA	840
Db 781	AATTTTACAGAAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCTTTATTGACAA	840
QY 841	TAAGTCTACAGAGGAGCTCTCTCAACCGGGGATATGTCAGAGGTGCTATCTGTC	900
Db 841	TAAGTCTACAGAGGAGCTCTCTCAACCGGGGATATGTCAGAGGTGCTATCTGTC	900
QY 901	TTATAAACTAGTACAGATATCTAAGTCTACCTCTCTGAAATCAGATGTTACTCTTCAG	960
Db 901	TTATAAACTAGTACAGATATCTAAGTCTACCTCTCTGAAATCAGATGTTACTCTTCAG	960
QY 961	CAACAATATATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGCTTC	1020
Db 961	CAACAATATATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGCTTC	1020
QY 1021	CGAGGAGCTTACCTTATTCAGTAGAAATAGTGTCAATGAGGTACAGCTCCTAAAGGTG	1080
Db 1021	CGAGGAGCTTACCTTATTCAGTAGAAATAGTGTCAATGAGGTACAGCTCCTAAAGGTG	1080
QY 1081	AGCCATAGCTATCGAAGATAGTGGGGAATTCAGTTTATCCGCCGATAGTGGTGAATGT	1140
Db 1081	AGCCATAGCTATCGAAGATAGTGGGGAATTCAGTTTATCCGCCGATAGTGGTGAATGT	1140
QY 1141	CTTTTATAGGAATACAGTCACTTCTCTCTCGGACGAATAGAAAGTATGATGCACTT	1200
Db 1141	CTTTTATAGGAATACAGTCACTTCTCTCTCGGACGAATAGAAAGTATGATGCACTT	1200
QY 1201	AGGAACGAGTGAAGATGACAGCTTCTGCTGCTGCTGAGCCATCTACTTCTA	1260
Db 1201	AGGAACGAGTGAAGATGACAGCTTCTGCTGCTGCTGAGCCATCTACTTCTA	1260
QY 1261	TGATCCCATTAATACAGGATCATCCAAACAGTTCACAGATGCTTAAAGTTAAAGAGAC	1320
Db 1261	TGATCCCATTAATACAGGATCATCCAAACAGTTCACAGATGCTTAAAGTTAAAGAGAC	1320
QY 1321	TCGGCAGATTTGCACTACATATACAGGGAACATCATCTTCAAGGAGAAAGTTATC	1380
Db 1321	TCGGCAGATTTGCACTACATATACAGGGAACATCATCTTCAAGGAGAAAGTTATC	1380
QY 1381	AGAGACAGAGCGCGAGATTTCAAAAATCTTCTGAGTCTACAGCTGCTGACTCT	1440
Db 1381	AGAGACAGAGCGCGAGATTTCAAAAATCTTCTGAGTCTACAGCTGCTGACTCT	1440
QY 1441	TTGAGGAGTACTCTATCTTTTAAACATGAGTGTCTCTGAGACTCAGGCAATTCAC	1500
Db 1441	TTGAGGAGTACTCTATCTTTTAAACATGAGTGTCTCTGAGACTCAGGCAATTCAC	1500
QY 1501	ACAGGAGATTTCTGCTCGAAATGAGCGTAGAACTCTCTAGAACCTTGCTGATCTAG	1560
Db 1501	ACAGGAGATTTCTGCTCGAAATGAGCGTAGAACTCTCTAGAACCTTGCTGATCTAG	1560
QY 1561	CACGATAACATTTGGTCATTAACATCAGTTCTTAGACGCTGCAAGAGCAAAAT	1620
Db 1561	CACGATAACATTTGGTCATTAACATCAGTTCTTAGACGCTGCAAGAGCAAAAT	1620
QY 1621	AGAAACCAAGCTACGTCAAAAAATCTGACTTTTCTGAAACCATCCTTTATTGACCC	1680
Db 1621	AGAAACCAAGCTACGTCAAAAAATCTGACTTTTCTGAAACCATCCTTTATTGACCC	1680
QY 1681	GACGGCAGCTTTTATGAAAAATCAGTTTAAAGAAATCTCAGTCTGACGATCTTAGA	1740
Db 1681	GACGGCAGCTTTTATGAAAAATCAGTTTAAAGAAATCTCAGTCTGACGATCTTAGA	1740
QY 1741	GCTCAAGCTCTCGAACTGTAAACAGCACCCAGTGTCTCAGATCTCTATATGAGTGA	1800
Db 1741	GCTCAAGCTCTCGAACTGTAAACAGCACCCAGTGTCTCAGATCTCTATATGAGTGA	1800
QY 1801	GAATTTCCATTACGGCTATCAGGGAATTTGGGGCCCAATTTGTTGGGGAGCAGGGCTTC	1860

Db 1801 GAAATTCATTACGGCTATCAGGGAACCTTGGGGCCCAATTTGTTGGGGGACAGGGGCTTC 1860
QY 1861 TAGACTGCAACCTTCAACTGGACTAAACTGGCTATATTCCTTAATCCCGAGGCTATCGG 1920
Db 1861 TAGACTGCAACCTTCAACTGGACTAAACTGGCTATATTCCTTAATCCCGAGGCTATCGG 1920
QY 1921 CTCTTTAGTCCCTTAATAGCTTATGGGAATGATTTATAGATATTAGTCTCTCCATTATCT 1980
Db 1921 CTCTTTAGTCCCTTAATAGCTTATGGGAATGATTTATAGATATTAGTCTCTCCATTATCT 1980
QY 1981 TATGGAGACTGCAAAACGAAAGGGTTGACGAGAGACCGTGTCTTTTGGTGTCTGGATTATC 2040
Db 1981 TATGGAGACTGCAAAACGAAAGGGTTGACGAGAGACCGTGTCTTTTGGTGTCTGGATTATC 2040
QY 2041 TAACCTTCTTCATAGATAGTACAAACACGACGCGGGTTTGGCCATTGAGTGGCGG 2100
Db 2041 TAACCTTCTTCATAGATAGTACAAACACGACGCGGGTTTGGCCATTGAGTGGCGG 2100
QY 2101 TTATGTCTATAGGAGGAAACCTACATCTCTTTCAGATAAGATCTTAGTCTGCTCATTTTG 2160
Db 2101 TTATGTCTATAGGAGGAAACCTACATCTCTTTCAGATAAGATCTTAGTCTGCTCATTTTG 2160
QY 2161 TCAGCTCTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGGTACAGTCTACGG 2220
Db 2161 TCAGCTCTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGGTACAGTCTACGG 2220
QY 2221 AGGAATCTCTATATACGACACAGCAACGAACTATATCTCTTCTTGGAACTACGGCC 2280
Db 2221 AGGAATCTCTATATACGACACAGCAACGAACTATATCTCTTCTTGGAACTACGGCC 2280
QY 2281 TTGTTGGTGTCTATGTCTTCTACAGAGATTCCTGTCTCTTTTCAGAAACCTTAGCTA 2340
Db 2281 TTGTTGGTGTCTATGTCTTCTACAGAGATTCCTGTCTCTTTTCAGAAACCTTAGCTA 2340
QY 2341 CACCCATACGATACGATCTGAAACCAAGTATACAAATATCCTACTCTTAAAGGAAG 2400
Db 2341 CACCCATACGATACGATCTGAAACCAAGTATACAAATATCCTACTCTTAAAGGAAG 2400
QY 2401 CTGGGGGATGATAGTTTGGCTTTAGAAATTCGGTGGAGAGCTCCGATTTGCTTAGATGA 2460
Db 2401 CTGGGGGATGATAGTTTGGCTTTAGAAATTCGGTGGAGAGCTCCGATTTGCTTAGATGA 2460
QY 2461 AAGTGTCTATTTGAGCAGTACATGCCCTTCATGAATTCAGTTTGTCTATGCACATCA 2520
Db 2461 AAGTGTCTATTTGAGCAGTACATGCCCTTCATGAATTCAGTTTGTCTATGCACATCA 2520
QY 2521 GGAAGGTTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTAGCCGTCTTTGTGA 2580
Db 2521 GGAAGGTTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTAGCCGTCTTTGTGA 2580
QY 2581 TCTTGCTTACCTATCGGATCCGATTTGATAGGATCAGATGCCAAGATCGAACGTA 2640
Db 2581 TCTTGCTTACCTATCGGATCCGATTTGATAGGATCAGATGCCAAGATCGAACGTA 2640
QY 2641 CAATCTAATCTTTGGTTATATCTGGATCTTGTTCGTAGTAACCCGACGTAGCACAAC 2700
Db 2641 CAATCTAATCTTTGGTTATATCTGGATCTTGTTCGTAGTAACCCGACGTAGCACAAC 2700
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Db 2701 ACTGCGAATAGCGGTGATTTCTGGAAAACTTCGGTACGAATTTGGCAAGACAAAGCTTT 2760
QY 2761 AGTCCTTCGTCAGGGAACCAATTTTCTTAACTCAAAATTTTGAAGCCTTTAGCCAAAT 2820
Db 2761 AGTCCTTCGTCAGGGAACCAATTTTCTTAACTCAAAATTTTGAAGCCTTTAGCCAAAT 2820
QY 2821 TTCTTTTGAATTCGTTGGGTCACTCCCAATTTACAATGTAGCTTAGGACCAAAATACCA 2880
Db 2821 TTCTTTTGAATTCGTTGGGTCACTCCCAATTTACAATGTAGCTTAGGACCAAAATACCA 2880
QY 2881 ATTCTAATCGTTAGCTTTGGTAAAGAGCTCCATACATCGAAGGGAAGAGCTTTTAAAG 2940
Db 2881 ATTCTAATCGTTAGCTTTGGTAAAGAGCTCCATACATCGAAGGGAAGAGCTTTTAAAG 2940

QY 2941 ATTTCTTGAAGGCTCTTTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTC 3000
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RESULT 2

AAx91990_00
WP Sequence split into 13 fragments LOCUS AAX91990 Accession Aax91990

Fragment Name	Begin	End
WP AAX91990_00	1	110000
WP AAX91990_01	100001	210000
WP AAX91990_02	200001	310000
WP AAX91990_03	300001	410000
WP AAX91990_04	400001	510000
WP AAX91990_05	500001	610000
WP AAX91990_06	600001	710000
WP AAX91990_07	700001	810000
WP AAX91990_08	800001	910000
WP AAX91990_09	900001	1010000
WP AAX91990_10	1000001	1110000
WP AAX91990_11	1100001	1210000
WP AAX91990_12	1200001	1230025

AAx91990 standard; DNA; 1230025 BP.

AC AAX91990;

XX 17-OCT-2003 (revised)

DT 13-SEP-1999 (first entry)

XX Nucleotide sequence of the complete genome of Chlamydia pneumoniae.

DE Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;

KW neutralising epitope; ss.

XX Chlamydothila pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

XX 21-NOV-1997; 97FR-00014673.

PR 04-NOV-1998; 98US-0107078P.

XX (GEST) GENSET.

XX Griffais R;

XX WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae.

PS Claim 1; Page 291-611; 1912pp; English.

XX The present sequence represents the complete genome of Chlamydia

CC pneumoniae, and encodes proteins AAX34584-Y35879. C. pneumoniae causes

CC respiratory disease such as pneumonia and bronchitis and is thought to be

CC a contributing factor in heart disease, sarcoidosis, sinusitis, purulent

CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded

CC by the open reading frames of the C. pneumoniae genome (see AAX34584-

CC Y35879) can be used in immunogenic compositions as vaccines. Vectors

CC containing C. pneumoniae nucleotide sequences can also be used as

CC immunogenic compositions, especially where the vector directs the

CC expression of a neutralising epitope of C. pneumoniae. (Updated on 17-OCT

XX -2003 to standardise OS field)

XX SQ Sequence 1230025 BP; 367213A; 249833C; 2498389T; 0U; 3770ther;

Query Match 99.2%; Score 2975.4; DB 2; Length 110000;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2998; Conservative 0; Mismatches 1; Indels 2; Gaps 2;			
Qy	1	CGCTCTTACCTAGTAGAGGTTGAGTGAATTTCTTGACTTGTGTTTCCCTATTGGTGTATCT	60
Db	31658	CGCTCTTACCTAGTAGAGGTTGAGTGAATTTCTTGACTTGTGTTTCCCTATTGGTGTATCT	31717
Qy	61	CTTAAATATTTAAATTCAAAATCAAAGTATATATTTTACAATGAAGTCTTCTTTCCCAA	120
Db	31718	CTTAAATATTTAAATTCAAAATCAAAGTATATATTTTACAATGAAGTCTTCTTTCCCAA	31777
Qy	121	GTGTTGATTTCTACATTTGCTATTTTCCCTTTGCTATGTTGCTACCGGACAGATTTT	180
Db	31778	GTGTTGATTTCTACATTTGCTATTTTCCCTTTGCTATGTTGCTACCGGACAGATTTT	31837
Qy	181	GGATTCAAAGTCGAGTTTCGATGGGAATAAAAATGGTAATTTTTCAGTTTCGTGAGAGTCA	240
Db	31838	GGATTCAAAGTCGAGTTTCGATGGGAATAAAAATGGTAATTTTTCAGTTTCGTGAGAGTCA	31897
Qy	241	GGAGATGCTGGAACTACTACCTATTTTAAGGGAATGTCACTCTAGAAAATATTCCTGG	300
Db	31898	GGAGATGCTGGAACTACTACCTATTTTAAGGGAATGTCACTCTAGAAAATATTCCTGG	31957
Qy	301	AACGGCACAGCAATCAGAAAAGCTGTTTAAACAACACTAAGGCGATTTGACTTTCCAC	360
Db	31958	AACGGCACAGCAATCAGAAAAGCTGTTTAAACAACACTAAGGCGATTTGACTTTCCAC	32017
Qy	361	AGTTAACGGGAACCTCTATTGTTCCAAAACGGTGGATGCAGGACTGTAGCAGGGGCTGC	420
Db	32018	AGTTAACGGGAACCTCTATTGTTCCAAAACGGTGGATGCAGGACTGTAGCAGGGGCTGC	32077
Qy	421	TGTTAAACGACGCTGGTAGATAAATCTACACAGTTTATAGGGTTTCTTCGCTATCTTT	480
Db	32078	TGTTAAACGACGCTGGTAGATAAATCTACACAGTTTATAGGGTTTCTTCGCTATCTTT	32137
Qy	481	TATTCGGTCTCTCGAAGTTCCGATAACTACCGCAAGAGCGCTTAGCTGCTCTACGGG	540
Db	32138	TATTCGGTCTCTCGAAGTTCCGATAACTACCGCAAGAGCGCTTAGCTGCTCTACGGG	32197
Qy	541	TAGCTTGAGTTTGACAAAATATGTCAGTTTGCTCTTCAGCAAAAATCTTTTCAACGGATAA	600
Db	32198	TAGCTTGAGTTTGAC- AAAAAATGTCAGTTTGCTCTTCAGCAAAAATCTTTTCAACGGATAA	32256
Qy	601	TGGCGGTGCTATCACCGCAAAATCTTTTCATTAAACAGGACTCAATGTCTAGCTCTGTT	660
Db	32257	TGGCGGTGCTATCACCGCAAAATCTTTTCATTAAACAGGACTCAATGTCTAGCTCTGTT	32316
Qy	661	TTCTGAAAATACCTCTCTCAAGAAAGGCGAGCCATTCAAGCTTCCGATGCCCTTACCAT	720
Db	32317	TTCTGAAAATACCTCTCTCAAGAAAGGCGAGCCATTCAAGCTTCCGATGCCCTTACCAT	32376
Qy	721	TACTGGAACCAAGGGAGTCTCTTTTCTGACAAATCTTCTTCGGATTTCTGGAGCTGC	780
Db	32377	TACTGGAACCAAGGGAGTCTCTTTTCTGACAAATCTTCTTCGGATTTCTGGAGCTGC	32436
Qy	781	AAATTTTACAGAGCTCGGTGACTATTCTTAATATGCTAAAGTTCTCTTTATTGACAA	840
Db	32437	AAATTTTACAGAGCTCGGTGACTATTCTTAATATGCTAAAGTTCTCTTTATTGACAA	32496
Qy	841	TAAAGTCTACAGAGCGAGCTCTCAACCAACGGGGATATGTCAAGAGGTGCTATCTGTGC	900
Db	32497	TAAAGTCTACAGAGCGAGCTCTCAACCAACGGGGATATGTCAAGAGGTGCTATCTGTGC	32556
Qy	901	TTATAAACTAGTACAGATACCTCACTGGAATCAGATGTTTACTCTTCAG	960
Db	32557	TTATAAACTAGTACAGATACCTCACTGGAATCAGATGTTTACTCTTCAG	32616
Qy	961	CAACATACATCGAACAGCGGAGGAGCTATCTATGTGAAAAGCTCGAATCGCTTC	1020
Db	32617	CAACATACATCGAACAGCGGAGGAGCTATCTATGTGAAAAGCTCGAATCGCTTC	32676
Qy	1021	CGAGGACTTACCTTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCTCTAAAGGTGG	1080
Db	32677	CGAGGACTTACCTTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCTCTAAAGGTGG	32736

Qy	1081	AGCCATAGCTATCGAAGATAGTGGGAATTCAGTTTATCCGCCGATAGTGTGACATTGT	1140
Db	32737	AGCCATAGCTATCGAAGATAGTGGGAATTCAGTTTATCCGCCGATAGTGTGACATTGT	32796
Qy	1141	CTTTTATAGGAATACAGTCACTTCTACTCTCTCGGAGCAATAGAAGTAGTATCGACTT	1200
Db	32797	CTTTTATAGGAATACAGTCACTTCTACTCTCTCGGAGCAATAGAAGTAGTATCGACTT	32856
Qy	1201	AGGAACGAGTGCAGAGATGACAGCTTTTCGCTTCTGCTGCTAGAGCATCTACTTCTA	1260
Db	32857	AGGAACGAGTGCAGAGATGACAGCTTTTCGCTTCTGCTGCTAGAGCACTACTTCTA	32916
Qy	1261	TGATCCCAATACTACAGGATCATCCAAACAGTTACAGATGTTTAAAGTTAATGAGAC	1320
Db	32917	TGATCCCAATACTACAGGATCATCCAAACAGTTACAGATGTTTAAAGTTAATGAGAC	32976
Qy	1321	TCGGCAGATTTCTGCACCTACAATATACAGGGAACATCATCTTTCACAGAGAAAAGTTATC	1380
Db	32977	TCGGCAGATTTCTGCACCTACAATATACAGGGAACATCATCTTTCACAGAGAAAAGTTATC	33036
Qy	1381	AGAGACAGAGCCGAGATTTCTAAAAATCTTACTTCGAAGCTACTACAGCCCTGTAACTCT	1440
Db	33037	AGAGACAGAGCCGAGATTTCTAAAAATCTTACTTCGAAGCTACTACAGCCCTGTAACTCT	33096
Qy	1441	TTTCAGGAGGTACTCTTATCTTTTAAACATGAGTGTACTCTGCAGACTCAGGCATTCACCTCA	1500
Db	33097	TTTCAGGAGGTACTCTTATCTTTTAAACATGAGTGTACTCTGCAGACTCAGGCATTCACCTCA	33156
Qy	1501	ACAGCAGATTTCTCGTCTCGAATGAGAGTAGGAATCTCTAGAACCTGCTGTACTAG	1560
Db	33157	ACAGCAGATTTCTCGTCTCGAATGAGAGTAGGAATCTCTAGAACCTGCTGTACTAG	33216
Qy	1561	CACCATAAACAAATTTGGTCTTAAACATCAGTTCTATAGACGCTGCAAAAGAGGCAAAAT	1620
Db	33217	CACCATAAACAAATTTGGTCTTAAACATCAGTTCTATAGACGCTGCAAAAGAGGCAAAAT	33276
Qy	1621	AGAAACCAAGTACGTCAGTCAAAATCTGACTTTTATCTGGAACCATCACTTTTATGACCC	1680
Db	33277	AGAAACCAAGTACGTCAGTCAAAATCTGACTTTTATCTGGAACCATCACTTTTATGACCC	33336
Qy	1681	GACGGCAGCTTTTATGAAAATCATAGTTTAAAGAAATCTCAGTCTCTACGACATCTAGA	1740
Db	33337	GACGGCAGCTTTTATGAAAATCATAGTTTAAAGAAATCTCAGTCTCTACGACATCTAGA	33396
Qy	1741	GCTCAAGCTTCTGGAACTGTAAACAGCACCGCAGTGAATCCATATATATGAGTGA	1800
Db	33397	GCTCAAGCTTCTGGAACTGTAAACAGCACCGCAGTGAATCCATATATATGAGTGA	33456
Qy	1801	GAAATTCATTTACGGCTATCAGGGAACCTTGGGGCCCAATTTGTTGGGGGACAGGGGCTTC	1860
Db	33457	GAAATTCATTTACGGCTATCAGGGAACCTTGGGGCCCAATTTGTTGGGGGACAGGGGCTTC	33516
Qy	1861	TACGACTGCAACCTTCAACTGACCTAAACCTGGCTATATTCCTAATCCGAGCGTATCGG	1920
Db	33517	TACGACTGCAACCTTCAACTGACCTAAACCTGGCTATATTCCTAATCCGAGCGTATCGG	33576
Qy	1921	CTCTTTAGTCCCTTAATAGCTTTATGGAATGCAATTTATAGATAATAGCTCTCTCCATTAAT	1980
Db	33577	CTCTTTAGTCCCTTAATAGCTTTATGGAATGCAATTTATAGATAATAGCTCTCTCCATTAAT	33636
Qy	1981	TATGAGACTGCAACAGAGGTTTCAGGAGACCGTCTGTTTTCGTTGCTGGATTAATC	2040
Db	33637	TATGAGACTGCAACAGAGGTTTCAGGAGACCGTCTGTTTTCGTTGCTGGATTAATC	33696
Qy	2041	TAACTTCTTCCATAAGGATAGTACAAAAACACAGCCGGGTTTCGCCAATTTGAGTGGCGG	2100
Db	33697	TAACTTCTTCCATAAGGATAGTACAAAAACACAGCCGGGTTTCGCCAATTTGAGTGGCGG	33756
Qy	2101	TTATGCTATAGAGGAAAACCTACATACCTTGTTCAGATAAGATCTTGTAGTGTGCAATTTTG	2160
Db	33757	TTATGCTATAGAGGAAAACCTACATACCTTGTTCAGATAAGATCTTGTAGTGTGCAATTTTG	33816

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QY 2161 TCAGCTCTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAATC-AAGGTACAGTCTACG 2219
|
|
|
Db 33817 TCAGCTCTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAATCAAAAGGTACAGTCTACG 33876
|
|
|
QY 2220 GAGGAATCTCTATTACAGACACAAACGAAACCTATATCTCTCTTCCCTTGCAAACTACGGC 2279
|
|
|
Db 33877 GAGGAATCTCTATTACAGACACAAACGAAACCTATATCTCTCTTCCCTTGCAAACTACGGC 33936
|
|
|
QY 2280 CTTGTTCTGTTGTCTATGTTCTTACAGAGATCTCTGTTCTCTTCTTTCAGGAAACCTTAGCT 2339
|
|
|
Db 33937 CTTGTTCTGTTGTCTATGTTCTTACAGAGATCTCTGTTCTCTTCTTTCAGGAAACCTTAGCT 33996
|
|
|
QY 2340 ACACCCATACGGATAACGATCTGAAACCAAGATATACAAATATCTCTACTCTGTTAAAGGAA 2399
|
|
|
Db 33997 ACACCCATACGGATAACGATCTGAAACCAAGATATACAAATATCTCTACTCTGTTAAAGGAA 34056
|
|
|
QY 2400 GCTGGGGGAATGATAGTTTCGTTTAGAATTCGGTGAAGAGTCCGATTTGCTTAGATG 2459
|
|
|
Db 34057 GCTGGGGGAATGATAGTTTCGTTTAGAATTCGGTGAAGAGTCCGATTTGCTTAGATG 34116
|
|
|
QY 2460 AAAGTGTCTATTAGCAGTACATGCCCTTCATGAATTTGCAATTTGCTATGTCACATC 2519
|
|
|
Db 34117 AAAGTGTCTATTAGCAGTACATGCCCTTCATGAATTTGCAATTTGCTATGTCACATC 34176
|
|
|
QY 2520 AGAAGGTTTAAAGAACAGGGAAACAGAGCTCGTGAATTTGGAAGTAGCCGCTTTGTGA 2579
|
|
|
Db 34177 AGAAGGTTTAAAGAACAGGGAAACAGAGCTCGTGAATTTGGAAGTAGCCGCTTTGTGA 34236
|
|
|
QY 2580 ATCTGCTTACCTATCGGATCGGATTTGATGAAGGATCAGACTGCCAGATGCAACGT 2639
|
|
|
Db 34237 ATCTGCTTACCTATCGGATCGGATTTGATGAAGGATCAGACTGCCAGATGCAACGT 34296
|
|
|
QY 2640 ACAATCTAACTCTTGGTTATCTACTGTGATCTTGTTCGTAGTAACCCCGACTGTACGACAA 2699
|
|
|
Db 34297 ACAATCTAACTCTTGGTTATCTACTGTGATCTTGTTCGTAGTAACCCCGACTGTACGACAA 34356
|
|
|
QY 2700 CACTGCGAATTACGGTGATTTCTTGGAACCTTCGGTAGCAATTTGGCAAGCAACAGCTT 2759
|
|
|
Db 34357 CACTGCGAATTACGGTGATTTCTTGGAACCTTCGGTAGCAATTTGGCAAGCAACAGCTT 34416
|
|
|
QY 2760 TAGTCCTTCGTGAGGAACCAATTTTGCTTTTAACCTAAATTTGAAGCCTTTAGCCAAT 2819
|
|
|
Db 34417 TAGTCCTTCGTGAGGAACCAATTTTGCTTTTAACCTAAATTTGAAGCCTTTAGCCAAT 34476
|
|
|
QY 2820 TTTCTTTTGAATTCGGTGGTCACTCGCAATTTACAAATGATAGACTTAGGAGCAAAATACC 2879
|
|
|
Db 34477 TTTCTTTTGAATTCGGTGGTCACTCGCAATTTACAAATGATAGACTTAGGAGCAAAATACC 34536
|
|
|
QY 2880 AATCTAAATCGTTAGCTTTGGTAAAGAGCTCCATACATCGAAGGGGAAAGAGCTTTTAA 2939
|
|
|
Db 34537 AATCTAAATCGTTAGCTTTGGTAAAGAGCTCCATACATCGAAGGGGAAAGAGCTTTTAA 34596
|
|
|
QY 2940 GATTCTCTGAGGCTCTTTTCGATTCGATTTCCATTTAGTTGTTTGTCTTAAACACTTT 2999
|
|
|
Db 34597 GATTCTCTGAGGCTCTTTTCGATTCGATTTCCATTTAGTTGTTTGTCTTAAACACTTT 34656
|
|
|
QY 3000 C 3000
|
|
|
Db 34657 C 34657
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RESULT 3

AAx06820

ID AAX06820 standard; DNA; 2787 BP.

XX

AC AAX06820;

XX

17-OCT-2003 (revised)

DT 26-APR-1999 (first entry)

XX

Chlamydia pneumoniae surface exposed protein Omp8 DNA.

DE

Omp8; outer membrane protein 8; surface exposed protein; antigen;

XX

KW infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX Chlamydophila pneumoniae.
OS
PN WO9858953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-DK000266.
XX
PR 23-JUN-1997; 97DX-00000744.
XX
PA (BIRK/) BIRKELUND S.
PA (CHRI/) CHRISTIANSEN G.
PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;
XX
DR WPI; 1999-105610/09.
DR P-PSDB; AAW88421.
XX
PT Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding these proteins.
XX
PS Claim 6; Page 52-53; 115pp; English.

This DNA sequence codes for the novel 90.0 kDa surface exposed protein Omp8 (see AAW88421) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see CAX06816-27) encoding Omp4-Omp15 proteins (see AAW88417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89.6-100.3 kDa and about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae. (Updated on 17-OCT-2003 to standardise OS field)

SQ Sequence 2787 BP; 811 A; 583 C; 598 G; 795 T; 0 U; 0 Other;

Query Match 92.5%; Score 2775.8; DB 2; Length 2787;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2780; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 101 ATGAGTCTTCTTTCCCAAGTTTGTATTTCTACATTTGCTATTTTCCCTTTGCTATG 160

Db 1 ATGAGTCTTCTTTCCCAAGTTTGTATTTCTACATTTGCTATTTTCCCTTTGCTATG 60

QY 161 ATTGCTACCGAGACAGTTTGGATTCAAGTGGAGTTTCGATGGGAATAAAATGTAAT 220

Db 61 ATTGCTACCGAGACAGTTTGGATTCAAGTGGAGTTTCGATGGGAATAAAATGTAAT 120

QY 221 TTTTCAGTTTCGTGAGTCCAGGAGATGCTGAACTACCTACCTATTTAAGGGAATGTC 280

Db 121 TTTTCAGTTTCGTGAGTCCAGGAGATGCTGAACTACCTACCTATTTAAGGGAATGTC 180

QY 281 ACTTAGAAAAATATTCCTCGAAACAGGCACAGCAATCAGAAAAAGCTGTTTAAACACACT 340

Db 181 ACTTAGAAAAATATTCCTCGAAACAGGCACAGCAATCAGAAAAAGCTGTTTAAACACACT 240

QY 341 AAGGGGATTTGACTTTTCAGTTACAGGTAAACGGGAACCTCTATTGTTTCAAACGGTGAATGA 400

Db 241 AAGGGGATTTGACTTTTCAGTTAAACGGGAACCTCTATTGTTTCAAACGGTGAATGA 300

QY	401	GGGACTGTACAGGGGCTGCTGTATAACAGCAGCGTGGTAGATAAACTCTACCAAGTTTATA	460	1381	CAGACTCAGGCATTCACTCAAAGCGCAGATTCTCGTCTCGAAATGGACGTAGGAACCTACT	1444	
DB	301	GGGACTGTACAGGGGCTGCTGTATAACAGCAGCGTGGTAGATAAACTCTACCAAGTTTATA	360	QY	1541	CTAGAAACCTTGCTGATACCTAGCACCATAAAACAATTTGGTCATTAAACATCAGTTCTATAGAC	1600
QY	461	GGGTTTCTTCGCTATCTTTTATTTGGCTCTCCCTGGAGTTTCGATAACTACCGGCAAGGA	520	DB	1441	CTAGRAACCTTGCTGATACCTAGCACCATAAAACAATTTGGTCATTAAACATCAGTTCTATAGAC	1500
DB	361	GGGTTTCTTCGCTATCTTTTATTTGGCTCTCCCTGGAAAGTTTCGATAACTACCGGCAAGGA	420	QY	1601	GGTGCAGAAAGGCAAAAAATAGAAAACCAAAAGCTACGTCAAAAATCTGACTTTATCTGGA	1660
QY	521	GCCGTTAGCTGCTCTACGGGTAGCTTCAGTTTGCAGAAAAATGTCAGTTTGCTCTTCAGC	580	DB	1501	GGTGCAGAAAGGCAAAAAATAGAAAACCAAAAGCTACGTCAAAAATCTGACTTTATCTGGA	1560
DB	421	GCCGTTAGCTGCTCTACGGGTAGCTTCGAGTTTGCAGAAAAATGTCAGTTTGCTCTTCAGC	480	QY	1661	ACCATCACCTTTATGGACCCGACGGCAGCTTTTATGAAAAATCATAGTTTAAAGAAATCCT	1720
QY	581	AAAAACCTTTCAACCGGATAATGGCGGTGCTATCAACCGCAAAAACTCTTTTCAATTAACAGGG	640	DB	1561	ACCATCACCTTTATGGACCCGACGGCAGCTTTTATGAAAAATCATAGTTTAAAGAAATCCT	1620
DB	481	AAAAACCTTTCAACCGGATAATGGCGGTGCTATCAACCGCAAAAACTCTTTTCAATTAACAGGG	540	QY	1721	CAGTCCCTACGACATCTTACAGAGCTCAAAGCTTCTGGAACCTGTAAACCAAGCAACCGCAGTGACT	1780
QY	641	ACTACAATGTCAGCTCTGTTTCTGAAAAATACCTCTCAAGAAAGCGGAGCCATTACG	700	DB	1621	CAGTCCCTACGACATCTTACAGAGCTCAAAGCTTCTGGAACCTGTAAACCAAGCAACCGCAGTGACT	1680
DB	541	ACTACAATGTCAGCTCTGTTTCTGAAAAATACCTCTCAAGAAAGCGGAGCCATTACG	600	QY	1781	CMAGATCTCTAATAATGGGTGAGAAAATTCATTACGGCTATCAGGGAACCTTTGGGGCCCAATT	1840
QY	701	ACTTCCGATGCCCTTACCAATTAATCTGGAAAACCAAGGGGAAGTCTCTTTTCTGCAATACT	760	DB	1681	CMAGATCTCTAATAATGGGTGAGAAAATTCATTACGGCTATCAGGGAACCTTTGGGGCCCAATT	1740
DB	601	ACTTCCGATGCCCTTACCAATTAATCTGGAAAACCAAGGGGAAGTCTCTTTTCTGCAATACT	660	QY	1841	GTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATT	1900
QY	761	TCCTTCGGATTCGAGGTGCAATTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCT	820	DB	1741	GTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATT	1800
DB	661	TCCTTCGGATTCGAGGTGCAATTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCT	720	QY	1901	CTTAATCCCGAGCGTATCGGCTCTTTTAGTCCCTTAATAGCTTATGGAATGCATTTATAGAT	1960
QY	821	AAAGTTTCCCTTATTGACATAAGGTACAGGAGCGAGCTCCTCAACAAAGGGGGATAG	880	DB	1801	CCTTAATCCCGAGCGTATCGGCTCTTTTAGTCCCTTAATAGCTTATGGAATGCATTTATAGAT	1860
DB	721	AAAGTTTCCCTTATTGACATAAGGTACAGGAGCGAGCTCCTCAACAAAGGGGGATAG	780	QY	1961	ATTAGTCTCTCCTATTCTTATGAGAGCTGCAACCAAGAGGTTGACAGGAGACCGTGCT	2020
QY	881	TCAGAGGTGCTATCTGTGCTTTATAAACTAGTACAGATCTAAAGTCAACCTCACTGGA	940	DB	1861	ATTAGTCTCTCCTATTCTTATGAGAGCTGCAACCAAGAGGTTGACAGGAGACCGTGCT	1920
DB	781	TCAGAGGTGCTATCTGTGCTTTATAAACTAGTACAGATCTAAAGTCAACCTCACTGGA	840	QY	2021	TTTTGGTGTGCTGGATTACTACTCTTCCATAAGGATAGTACAAAAACACGACGCGGG	2080
QY	941	AATCAGATGTTACTCTTCAGCAACAATACATCGACAACAGCGGAGGAGCTATCTATGT	1000	DB	1921	TTTTGGTGTGCTGGATTACTACTCTTCCATAAGGATAGTACAAAAACACGACGCGGG	1980
DB	841	AATCAGATGTTACTCTTCAGCAACAATACATCGACAACAGCGGAGGAGCTATCTATGT	900	QY	2081	TTTTGGTGTGCTGGATTACTACTCTTCCATAAGGATAGTACAAAAACACGACGCGGG	2140
QY	1001	AAAAAGCTCGAAGTGGCTTCGGAGGACTTACCTTATTCAGTAGAATAGTGTCAATGGA	1060	DB	1981	TTTTGGTGTGCTGGATTACTACTCTTCCATAAGGATAGTACAAAAACACGACGCGGG	2040
DB	901	AAAAAGCTCGAAGTGGCTTCGGAGGACTTACCTTATTCAGTAGAATAGTGTCAATGGA	960	QY	2141	ATTTCCGCAATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAG	2200
QY	1061	GGTACAGCTCTTAAAGTGGAGCCATAGCTATCGAAGATAGTGGGAATTCAGTTTATCC	1120	DB	2041	ATTTCCGCAATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAG	2100
DB	961	GGTACAGCTCTTAAAGTGGAGCCATAGCTATCGAAGATAGTGGGAATTCAGTTTATCC	1020	QY	2201	AATTCAGGTACAGTCTACCGGAGGAACTCTCTATTACCAGCACAAACGAACCTATATCTCT	2260
QY	1121	GCCGATAGTGGTGACATTTCTTTTAGGGAATACAGTCACTTCTACTCTCCCTGGGAGC	1180	DB	2101	AATTCAGGTACAGTCTACCGGAGGAACTCTCTATTACCAGCACAAACGAACCTATATCTCT	2160
DB	1021	GCCGATAGTGGTGACATTTCTTTTAGGGAATACAGTCACTTCTACTCTCCCTGGGAGC	1080	QY	2261	CTTCCCTTGCAAACTACGGCCCTTGTTCGTTGCTTATGTTCTCCTACAGAGATTCCTGTTCTC	2320
QY	1181	AATAGAAGTAGTATCGACTTAGGAACGAGTCCGAAGATGACAGCTTTGCGTTCTGCTGCT	1240	DB	2161	CTTCCCTTGCAAACTACGGCCCTTGTTCGTTGCTTATGTTCTCCTACAGAGATTCCTGTTCTC	2220
DB	1081	AATAGAAGTAGTATCGACTTAGGAACGAGTCCGAAGATGACAGCTTTGCGTTCTGCTGCT	1140	QY	2321	TTTTTCAGAAAACCTTAGCTACACCCATACCGATACGATCTGAAAAACCAAGTATACACA	2380
QY	1241	GGTAGAGCCATCTACTCTATGATCCCACTACTACAGGATCATCCACAACAGTGTACAGAT	1300	DB	2221	TTTTTCAGAAAACCTTAGCTACACCCATACCGATACGATCTGAAAAACCAAGTATACACA	2280
DB	1141	GGTAGAGCCATCTACTCTATGATCCCACTACTACAGGATCATCCACAACAGTGTACAGAT	1200	QY	2381	TATCCTACTCTTAAAGGAAGCTCGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGGAAAG	2440
QY	1301	GTCTTTAAAGTTAATGAGACTCCGGCAGATTCGCACTTACAAATATACAGGGAACATCATC	1360	DB	2281	TATCCTACTCTTAAAGGAAGCTCGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGGAAAG	2340
DB	1201	GTCTTTAAAGTTAATGAGACTCCGGCAGATTCGCACTTACAAATATACAGGGAACATCATC	1260	QY	2441	GCTCCGATTTGCTTAGATGAAAGTGTCTTATTTGAGCAGTACATGCCCTTCATGAAATTCG	2500
QY	1361	TTACAGGAGAAAAGTTATCAGAGACAGAGGCGCGAGTTCTTAAATCTTACTTCGAG	1420	DB	2341	GCTCCGATTTGCTTAGATGAAAGTGTCTTATTTGAGCAGTACATGCCCTTCATGAAATTCG	2400
DB</							

Db 2461 GGAAGTAGCGCTTCTGTGAATCTTGCTTACCTATCGGGATCCGATTTGATAGGAATCA 2520
 QY 2621 GACTGCCAAGATGCAACGATCAATCTAACTCTTGGTTATCTGTGGATCTTGTTCGTAGT 2680
 Db 2521 GACTGCCAAGATGCAACGATCAATCTAACTCTTGGTTATCTGTGGATCTTGTTCGTAGT 2580
 QY 2681 AACCCGACTGTACGACACACACTGCGAATTAGCGGTGATTTCTTGGAAAACCTTTCGGTACG 2740
 Db 2581 AACCCGACTGTACGACACACACTGCGAATTAGCGGTGATTTCTTGGAAAACCTTTCGGTACG 2640
 QY 2741 AATTGGCAAGCAAGCTTTAGTCTTCTTGGTGGAGAACCAATTTTGTCTTAACTCAAAAT 2800
 Db 2641 AATTGGCAAGCAAGCTTTAGTCTTCTTGGTGGAGAACCAATTTTGTCTTAACTCAAAAT 2700
 QY 2801 TTTGAGCCTTTAGCCAAATTTCTTTTGAATTTGGTGGTGCATCTCGCAATTACAATGTA 2860
 Db 2701 TTTGAGCCTTTAGCCAAATTTCTTTTGAATTTGGTGGTGCATCTCGCAATTACAATGTA 2760
 QY 2861 GACTTAGGAGCAAAATACCAATTTCTAA 2887
 Db 2761 GACTTAGGAGCAAAATACCAATTTCTAA 2787

RESULT 4

ABL91193

ID ABL91193 standard; DNA; 2241 BP.

XX ABL91193;

AC ABL91193;

XX ABL91193;

XX ABL91193;

XX ABL91193;

XX ABL91193;

XX ABL91193;

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XX ABL91193;

XX ABL91193;

XX ABL91193;

PS Claim 5; Page 50; 364pp; English.

XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 2241 BP; 660 A; 475 C; 478 G; 628 T; 0 U; 0 Other;

Query Match 74.7%; Score 2241; DB 6; Length 2241;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 ATGTCAGCTCTGTTTCTGAAATACCTCTCAAGAAAGCGGAGCCATTCAGACTTC 706
 Db 1 ATGTCAGCTCTGTTTCTGAAATACCTCTCAAGAAAGCGGAGCCATTCAGACTTC 60
 QY 707 GATGCCCTTACCATTACTGTGAACCAAGGGAAGTCTCTTTTCTGACATACTTCTTCG 765
 Db 61 GATGCCCTTACCATTACTGTGAACCAAGGGAAGTCTCTTTTCTGACATACTTCTTCG 120
 QY 767 GATCTGGAGTGCATTTTACAGAAAGCTCGGTGACTATTTCTAATAATGCTAAAGTT 826
 Db 121 GATCTGGAGTGCATTTTACAGAAAGCTCGGTGACTATTTCTAATAATGCTAAAGTT 180
 QY 827 TCCTTTATTGACAAATAGGTACAGAGGCGAGTCTCTCAACACGGGGGATATCTCAGGA 886
 Db 181 TCCTTTATTGACAAATAGGTACAGAGGCGAGTCTCTCAACACGGGGGATATCTCAGGA 240
 QY 887 GGTGCTATCTGTCTTATAAACTAGTACAGATACTAAAGTCACTCCCTCACTGAAATCAG 946
 Db 241 GGTGCTATCTGTCTTATAAACTAGTACAGATACTAAAGTCACTCCCTCACTGAAATCAG 300
 QY 947 ATGTTACTCTTACAGCAACAATACATGCAACAGCGGGAGAGTCTATGTGAAAAG 1006
 Db 301 ATGTTACTCTTACAGCAACAATACATGCAACAGCGGGAGAGTCTATGTGAAAAG 360
 QY 1007 CTCGAACTGGCTTCCGGAGGACTTACCCTATTTCAGTAGAATAGTGTCAATGGAGGTACA 1066
 Db 361 CTCGAACTGGCTTCCGGAGGACTTACCCTATTTCAGTAGAATAGTGTCAATGGAGGTACA 420
 QY 1067 GCTCCTAAAGTGGAGCCATAGCTATCGAAGATAGTGGGAATTTGAGTTTATCCGCCAT 1126
 Db 421 GCTCCTAAAGTGGAGCCATAGCTATCGAAGATAGTGGGAATTTGAGTTTATCCGCCAT 480
 QY 1127 AGTGGTGACATTTCTTTTATAGGAATACAGTCACTTCTACTCTCTCTGGGACGAATAGA 1186
 Db 481 AGTGGTGACATTTCTTTTATAGGAATACAGTCACTTCTACTCTCTCTGGGACGAATAGA 540
 QY 1187 AGTAGTATCGACTTAGGACGAGTGCAGATACAGCTTTTGGCTTCTGCTGGGTAGA 1246
 Db 541 AGTAGTATCGACTTAGGACGAGTGCAGATACAGCTTTTGGCTTCTGCTGGGTAGA 600
 QY 1247 GCCATCTTCTATGATCCATAAATACAGGATCATCCAAACAGTTACAGATGTCTTA 1306
 Db 601 GCCATCTTCTATGATCCATAAATACAGGATCATCCAAACAGTTACAGATGTCTTA 660
 QY 1307 AAGATTAAAGACTCCGGCAGATTTCTGACTACATATACAGGAAACATCTTCTTCA 1366
 Db 661 AAGATTAAAGACTCCGGCAGATTTCTGACTACATATACAGGAAACATCTTCTTCA 720

Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
 XX

QY 1367 GGAGAAAAGTTATCAGAGACAGAGCCGAGATTCCTAAATCTTACCTCGAAGCTACTA 1426
Db 721 GGAGAAAAGTTATCAGAGACAGAGCCGAGATTCCTAAATCTTACCTCGAAGCTACTA 780
QY 1427 GAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAACATCGAGTGAATCTCGAGACT 1486
Db 781 GAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAACATCGAGTGAATCTCGAGACT 840
QY 1487 CAGGCATTCACTCAACAGCAGCATCTCGTCTCGAAATGGAGTGGAACTACTCTAGAA 1546
Db 841 CAGGCATTCACTCAACAGCAGCATCTCGTCTCGAAATGGAGTGGAACTACTCTAGAA 900
QY 1547 CTTCTGTGATPACTAGCACCATAAACAAATTTGGTCATTAAACATCAGTTCTATAGACGGTGCA 1606
Db 901 CTTCTGTGATPACTAGCACCATAAACAAATTTGGTCATTAAACATCAGTTCTATAGACGGTGCA 960
QY 1607 AAGAGGCGAAAATAGAACCAAGCTAGCTCAAAAATCTGACATTTATCTGGAACCATC 1666
Db 961 AAGAGGCGAAAATAGAACCAAGCTAGCTCAAAAATCTGACATTTATCTGGAACCATC 1020
QY 1667 ACTTTATTGGACCCGACGGGACGTTTTATGAAATCATAGTTTAAAGAAATCTCAGTCC 1726
Db 1021 ACTTTATTGGACCCGACGGGACGTTTTATGAAATCATAGTTTAAAGAAATCTCAGTCC 1080
QY 1727 TAGCAGATCTTAGAGCTCAAGCTTCTGGAATCTGAACTGTAACAGCACCGCAGTGAATCCAGAT 1786
Db 1081 TAGCAGATCTTAGAGCTCAAGCTTCTGGAATCTGAACTGTAACAGCACCGCAGTGAATCCAGAT 1140
QY 1787 CTTAATAGGGTGAGAAATTCATTTACGGCTATCAGGAACTGGGGCCCAATTTGTTGG 1846
Db 1141 CTTAATAGGGTGAGAAATTCATTTACGGCTATCAGGAACTGGGGCCCAATTTGTTGG 1200
QY 1847 GGGACAGGGGCTTCTACGACTGCAACCTTCACTGGACTTAAACCTGGCTATATCTCTAAT 1906
Db 1201 GGGACAGGGGCTTCTACGACTGCAACCTTCACTGGACTTAAACCTGGCTATATCTCTAAT 1260
QY 1907 CCGGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGC 1966
Db 1261 CCGGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGC 1320
QY 1967 TCTCTCCATTAATCTTATGAGACTGCAACGAGGAGGTTGCGGGAGACGGCTCTTTTGG 2026
Db 1321 TCTCTCCATTAATCTTATGAGACTGCAACGAGGAGGTTGCGGGAGACGGCTCTTTTGG 1380
QY 2027 TGTCTGGAATTAATCTTCTTCCATAGGATAGTACAAAACACGACGCGGGTTTCGC 2086
Db 1381 TGTCTGGAATTAATCTTCTTCCATAGGATAGTACAAAACACGACGCGGGTTTCGC 1440
QY 2087 CATTTGAGTGGCGGTTATGTCTAGAGGAAACCTTACATCTTGTTCAGATTAAGATTCTT 2146
Db 1441 CATTTGAGTGGCGGTTATGTCTAGAGGAAACCTTACATCTTGTTCAGATTAAGATTCTT 1500
QY 2147 AGTGTCTGATTTTGTTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGATCAA 2206
Db 1501 AGTGTCTGATTTTGTTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGATCAA 1560
QY 2207 GGTACAGTCTACGGAGAACTCTCTATTACAGCACAAACGAAACCTTATCTCTCTCTCT 2266
Db 1561 GGTACAGTCTACGGAGAACTCTCTATTACAGCACAAACGAAACCTTATCTCTCTCTCT 1620
QY 2267 TGCAACTACGGCCTTGTTCGTTGCTTATGTTCTTACAGATTCCTGTTCTCTTTTCA 2326
Db 1621 TGCAACTACGGCCTTGTTCGTTGCTTATGTTCTTACAGATTCCTGTTCTCTTTTCA 1680
QY 2327 GGAACCTTTAGCTACACCCATACGGATACGATCTGAAACCAAGTATACACATATCT 2386
Db 1681 GGAACCTTTAGCTACACCCATACGGATACGATCTGAAACCAAGTATACACATATCT 1740
QY 2387 ACTGTTAAAGAGCTGGGGGAATGATAGTTTCGTTTGAATTCGGTGGAAAGACTCG 2446
Db 1741 ACTGTTAAAGAGCTGGGGGAATGATAGTTTCGTTTGAATTCGGTGGAAAGACTCG 1800

QY 2447 ATTCTCTAGATGAAAGTGTCTTATTGAGCAGTACATGCCCTTCATGAAATTCGAGTTT 2506
Db 1801 ATTCTCTTAGATGAAAGTGTCTTATTGAGCAGTACATGCCCTTCATGAAATTCGAGTTT 1860
QY 2507 GTCTATGCACATCAGAAAGGTTTTAAAGAACAGGGAACAGAGCTCGTGAATTCGAAGT 2566
Db 1861 GTCTATGCACATCAGAAAGGTTTTAAAGAACAGGGAACAGAGCTCGTGAATTCGAAGT 1920
QY 2567 AGCCCTCTTGTGAATCTTTCGCCCTTACTATCGGGATCCGATTTGATAAGGAATCAGACTGC 2626
Db 1921 AGCCCTCTTGTGAATCTTTCGCCCTTACTATCGGGATCCGATTTGATAAGGAATCAGACTGC 1980
QY 2627 CAAGATGCAACGTACAACTAACTCTTGGTTATATCTGTGGATCTTGTTCGTAGTAAACCCC 2686
Db 1981 CAAGATGCAACGTACAACTAACTCTTGGTTATATCTGTGGATCTTGTTCGTAGTAAACCCC 2040
QY 2687 GACTCTACGACAACTCGGATTTAGCGGTGATTTCTTGGAAACCTTCGGTACGAATTTG 2746
Db 2041 GACTCTACGACAACTCGGATTTAGCGGTGATTTCTTGGAAACCTTCGGTACGAATTTG 2100
QY 2747 GCAAGACAAGCTTTTACTCTTCTGTCAGGGAACCAATTTTGTCTTAACTCAAATTTTGA 2806
Db 2101 GCAAGACAAGCTTTTACTCTTCTGTCAGGGAACCAATTTTGTCTTAACTCAAATTTTGA 2160
QY 2807 GCCTTTAGCCAAATTTTCTTTTGAATTTGCGTGGGTCACTCGCAATTAAGTGTAGACTTA 2866
Db 2161 GCCTTTAGCCAAATTTTCTTTTGAATTTGCGTGGGTCACTCGCAATTAAGTGTAGACTTA 2220
QY 2867 GGAGCAAAATACCAATTTCTAA 2887
Db 2221 GGAGCAAAATACCAATTTCTAA 2241
RESULT 5
AB084775
ID AB084775 standard; DNA; 2781 BP.
XX AB084775;
AC AC
XX 29-AUG-2003 (revised)
DT 25-FEB-2003 (first entry)
XX Chlamydia psittaci antigen CP4#12 encoding DNA SEQ ID NO:56.
DE Chlamydia psittaci; vaccination; vaccine; antigen; immune response;
KW immunisation; antibacterial; infection; gene; ds.
XX Chlamydia caviae.
XX OS
FH Key Location/Qualifiers
FT CDS 1..2781
FT /*tag= a
FT /product= "antigen CP4#12"
XX
XX WO200253588-A2.
XX
XX 11-JUL-2002.
XX
XX 17-DEC-2001; 2001WO-US048715.
XX
XX 15-DEC-2000; 2000US-00738269.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Johnston SA, Stemke-Hale K, Sykes KF, Kaltenboeck B;
XX
XX WPI; 2002-537942/57.
XX P-PSDB; ABP56019.
XX
XX Vaccine for immunization of animal, preferably bovine, against Chlamydia
PT psittaci, comprises at least one polynucleotide having a C. psittaci
PT sequence, or at least one C. psittaci antigen.

Db 2115 TGTATATTATCAGCATGTGAGCAAGTTGATGATCTCAGCGGTTATTTATATGGCCCTAA 2174
QY 2281 TTGTTTCGTTGCTTATGTTCTTACAGAGATTCCTGTTCTCTTTTTCAGGAAACCTTTAGCTA 2340
Db 2175 CACGTGTTGTTTCAGGGTTTCTTAAGAGATTCCTATTTTCTGGATGACAAATACCTA 2234
QY 2341 CACCATACGGATAACGATCTGAAACCAAGTATACAAATATCTCTGTTAAAGGAAG 2400
Db 2235 TTGCACACACGGCCAAACATGACACACGCTCTATACAGACTATCTGAAGTGAAGGTTTC 2294
QY 2401 CTGGGGGAATGATAGTTTTCGCTTTTGAATTCGGTGAAGAGCTCCGATTTGCTTAGATCA 2460
Db 2295 TTGGGGTAATGATACCTCGGGCTTAACCTTTGCTACTAGCGTACCTATCCCGGTTATTTAG 2354
QY 2461 AAGTCTCTATTTGACAGTACATGCCCTTTCATGAAATTCGCAATTTGCTATGCAATCA 2520
Db 2355 TTCTCTATCTTTGATGTTATGTCACCGTTTGCATAATTTACAAGTTGCTATGCGCACCA 2414
QY 2521 GGAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTAGCCGCTTTGTGAA 2580
Db 2415 AGATGACTTTAAAGAACCAACACAGAGCGCGGCTTTTGAAGCAGCGATCTTCTCAA 2474
QY 2581 TCTTCGCTTACCTATCTCGGATCCGATTTGATAGGAATTCAGACTGCCAAGTGCACGTA 2640
Db 2475 CGTTTCTGTACTATAGGTATATAAATTTGAGAACTCTCTATGAGAGAGAGTGTCTTA 2534
QY 2641 CAATCTAACTCTTGTGTATCTGATCTGTTGTTGTTAGTAAACCCGACTGTACGACAA 2700
Db 2535 TGACTTTACACTGATATATACCTGATGTGTACCGTCAATATCCAAGCTGTATGACAGG 2594
QY 2701 ACTGGAATTTAGCGGTGATCTTGGAACCTTCGGTAGCAATTTGGCAAGCAAGCTTTT 2760
Db 2595 ATTGGCGATCAATGACGTTTCTCGGTTTAAACAGACTACCAATCTTGTGTAGCAAGCTTT 2654
QY 2761 AGTCCTTCTGTCAGGGAACCATTTTGTCTTAACTCAAAATTTTGAAGCCTTTTGAACAATT 2820
Db 2655 CATAGTTCCGCGGTAAACATATTTGCTTAACTTAACTTAACTTAACTTAACTTAACTT 2714
QY 2821 TTCTTTTGAATTCGTTGGTCTATCTGCAATTTACAAATTTAGAGTGTAGGAGCAAAATACA 2880
Db 2715 TGGTTTCGAATTTACGAAGCTCTTCAAGAAATTTAAGCTAGATCTTGGCGCTAAGTCTGC 2774
QY 2881 ATTCTAA 2887
Db 2775 GTTCTAA 2781

RESULT 6

ABQ78033

ID ABQ78033 standard; DNA; 2781 BP.

XX AC

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WPI; 2002-583472/62.

P-PSDB; ABB98228.

Vaccine useful for immunizing an animal, comprising at least one polynucleotide having a Chlamydia sequence or at least one Chlamydia antigen.

Claim 6; Page 167-168; 183pp; English.

The invention relates to a vaccine (I) comprising at least one polynucleotide (ABQ78008-ABQ78039) having a Chlamydia sequence or at least one Chlamydia antigen (ABB98203-ABB98234) and a pharmaceutically acceptable carrier. The antigens are useful for immunising an animal, by providing at least one Chlamydia antigen or its antigenic fragment to the animal, in an amount effective to induce an immune response in the animal e.g. mammals including bovine or human. The method is effective to induce an immune response against C. psittaci, C. pneumoniae or non-Chlamydia infection. The method further involves administering to the animal an antigen or an antigenic fragment from Chlamydia species other than C. psittaci or C. pneumoniae or an antigenic fragment from a non-Chlamydia species. (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 2781 BP; 818 A; 555 C; 610 G; 798 T; 0 U; 0 Other;

Query Match 18.2%; Score 546.6; DB 6; Length 2781;

Best Local Similarity 53.7%; Pred. No. 8.8e-141;

Matches 1390; Conservative 0; Mismatches 1134; Indels 63; Gaps 10;

QY 328 TTTTAAACACTAAGGCGGATTCACCTTTTACAGGTAACGGAACTCTCTATTGTTCCA 387

Db 231 TTTTTCAGACTGCGAGACACCTAACTTTTCAAGGGAACACCATAGCTTATCCATAAC 290

QY 388 AACGCTGATGACGAGGACTGTAGCAGGGGCTGCTTTAAACAGCAGCGGTAGATAAATC 447

Db 291 GBAACGGAATGCGGAGCTAATCC---TGCGGAATTAACGTTAACACTGCCGATAAGAT 347

QY 448 TACACGTTTATAGGGTTTCTTCGCTATCTTTTATGCGTCTCTCGGAAGTTTCGATAC 507

Db 348 TCTTACGCTGACAGATTTTCTTAAGTTGAGCTTTAAGGAATGCCCATCTCTCTAGTAA 407

QY 508 TACCGGCAAGGAGCGGTAGCTGCTTACGGGTAGCTTGTGTTGACAAAAATGTCAG 567

Db 408 TACTGGAAGAGGGGC---TATGAATCCGAGGAGCATTAAACTTAGCGAATATGCCAG 464

QY 568 TTTGCTCTTCAGCAAAAATTTTCAACGGAATATGCGGTGCTATCACGCCAAAATCT 627

Db 465 TATTCCTGTTTATGATCAGAACTATTCGCTGAGAATGGTGAGGCACTCTCTTGCAGGCTTT 524

QY 628 TTCATTACAGGAGCTACAAATGCTAGCTCTGTTTCTGAAATACCTCTCTCAAGAAAGG 687

Db 525 TTTCTTAACCGGCTCGAGCAAGAAATCAGCTTTCACCACTAACTCTACTGCGAAAAAGG 584

QY 688 CGGAGCAATTCAGACTTCGAGTCCCTTACCACTTACGAAACCAAGGGAAGTCTCTTT 747

Db 585 TGGAGGATTTGCTGCTACGGGAATAGCTCATCTTTTGGCAACCAAGGCAATCAGATT 644

QY 748 TTTTCACAAATCTCTTCGGATTCTGGAGTCAATTTTACAGAGCCTCGGTGACTAT 807

Db 645 TTTCTGGAACACTGCTGTGAATTTCTGGGGAGCAGTATATTTCAGAAAGCTTCTATGAGAT 704

QY 808 TTTCTAATATGCTAAAGTTTCTTTTATTTGAATTAAGTTCACAGAGGAGTCTCTCAAC 867

Db 705 TGCAGGTAAACACCACTGCTTTTATGCAACAACTGCTTTTCGGGTTCACTCT- 756

QY 868 AACGGGGATATGTCAGGAGGTGCTATCTGTCTTATAAACTAGTACAGATCTAAGGT 927

Db 757 -----GATGGTTGCGGTGGAGCTATCCATTGTAGCAAAACAGGTTAGCCGCCCT 809

QY 928 CACCTCTACATGGAATCAGATTTACTCTTACAGCAACATATCATCAACACGCGGAGG 987

Db 810 TACTATAGAGATAACAAAGTCTTGTATTTTTCAGGGAATACTTCTTTCAGAAAGGTGG 869

community-acquired pneumonia; coronary heart disease.

Chlamydophila caviae.

US2002183272-A1.

05-DEC-2002.

17-DEC-2001; 2001US-00023437.

16-AUG-2000; 2000US-0225839P.

(JOHN/) JOHNSTON S A.

(STEM/) STEMKE-HALE K.

(SYKE/) SYKES K F.

(KALT/) KALTENBOECK B.

Johnston SA, Stemke-Hale K, Sykes KF, Kaltenboeck B;

WPI: 2003-328634/31.

P-PSDB; ABU66284.

New vaccine comprising a polynucleotide with a Chlamydia sequence or a Chlamydia antigen, for inducing an immune response against Chlamydia psittaci, Chlamydia pneumoniae, other Chlamydia species, or a non-Chlamydia infection.

Claim 6: Page 74-76: 100pp: English:

The invention relates to a vaccine comprising a pharmaceutical carrier and at least one polynucleotide having a Chlamydia sequence or at least one Chlamydia antigen. The polynucleotide sequences are obtained from a cloned expression library of fragmented genomic DNA (expressed in the vector pCMV-Ubi (+p3)). Also included are immunising an animal comprising providing to the animal at least one Chlamydia antigen or its antigenic fragment (expressed from the cloned polynucleotides) to induce an immune response (the proteins are chosen by transforming a vertebrate animal with constituents of the library and choosing those which elicit the best immune response, and then expressing those clones in cell culture and purifying the protein), preparing antibodies against a Chlamydia antigen (comprising identifying a Chlamydia antigen that confers immune resistance against chlamydia bacterial infection when challenged with the Chlamydia species in which the antigen was prepared, generating an immune response in a vertebrate animal with the identified antigen, and obtaining antibodies produced in the animal, the antibodies are used to assay for the presence of chlamydia infection in a vertebrate animal) and testing for antigens for a first disease state/infectious agent (comprising determining an antigenic polypeptide or a nucleic acid encoding an antigenic polypeptide from a second disease state or infectious agent, obtaining a homologue of the antigenic polypeptide or a nucleic acid encoding an antigenic polypeptide from a second disease state or infectious agent for the first disease state/infectious agent, and testing the homology to see if it is an antigenic polypeptide or a nucleic acid encoding an antigenic polypeptide for the first disease state or infectious agent). The vaccine, antigens and polynucleotides are useful for inducing a protective immune response in vertebrate animals against *C. psittaci*, *C. pneumoniae*, other species of Chlamydia, or a non-Chlamydia infection. The antigens are also useful for antibody preparation techniques. Chlamydia species are responsible for blindness, sexually transmitted disease, community-acquired pneumonia and act as cofactors in atherosclerotic plaque formation in coronary heart disease. *C. psittaci* in particular is a cause of mastitis, infertility and abortion in cattle. The present sequence is one of the cloned chlamydia psittaci genomic DNA fragments of the invention. (Updated on 27-OCT-2003 to standardise OS field)

Sequence 2781 BP; 818 A; 555 C; 610 G; 798 T; 0 U; 0 Other:

ery Match
18.2%; Score 546.6; DB 7; Length 2781;

st Local Similarity 53.7%; Pred. No. 8.8e-141;

Matches 1390; Conservative 0; Mismatches 1134; Indels 63; Gaps 10;

328 TTTTAAACAACACTAAGGGGATTGACTTTCACAGGTACGGGAACCTCTATTGTCCA 387

[illegible]

Db 1275 TAACCTAAAGACAAATTTACACAGCCTATCACTTTAGCTGCTGGTGAACCTTGTGTTAAG 1334
QY 1465 ACATGAGTGACTCTCGCAGACTCAGGCAATTCATCTCAACAGGCGAGTCTCGTCTCGAAT 1524
Db 1335 CACGGGTGTGGAAAGTAGAAGCAAAACAGTCGTCGAACACAGCAGGATCTTTGATTTCTGAT 1394
QY 1525 GGACGTGAGGAACCTACTCTA---GAACCTGCTGATCTAGCACCATAAACAATTTGGTTCAT 1581
Db 1395 GGATGACGGCAAAAGTTATCCGCAAAAACAGAGATGCTCACTGACGAATCTGGCTAT 1454
QY 1582 TAACATCAGTTCTATAGACGGTCAAAAGAGGCAAAAATAGAACCAAAAGCTACGTCAAA 1641
Db 1455 TAATCCGAATACCTTAGATGGGAAAAAATTCGCGTAGTCGATGCGCTTCTGCTGGGAA 1514
QY 1642 AATCTGACTTTTATCTGGAACCATCTTTATTTGGACCCGACGGGACGTTTATGAAA 1701
Db 1515 GAATGTGACTTTATCAGGTCTATTTGGCGTTATTTGATCCTACAGGGGAAGTTTATGAAA 1574
QY 1702 TCATAGTTTAAAGAAATCCTCAGTCCTACGACATCTTAGAGCTCAAGACTTCTCGAACTGT 1761
Db 1575 CCATAGCTAAATGATAGTTAGTTTAGAGGAATTCACATTTCTGGGAAAGTTCCGT 1634
QY 1762 AACAAACACCGCAGTGTCTCAGATCCTAATATGAGGAGGAGAAATTCATACGGCTATCA 1821
Db 1635 GACAAACCAACGTCCTAGTCATGTTGTTGTTGTTGCTGAAACCCACTATGTTATCA 1694
QY 1822 GGGAAAC-----TTGGGGCCCAATTTGTTGGGGACAGGGGCTTCTAGGACTGC 1869
Db 1695 AGGAAACTGCTGTCTAGTTGGGTCAAGATAATAACTCTGATCCTAANAACAAACAGC 1754
QY 1870 AACCTCAACTGACTAAAACTGCTATATTCCTAATCCGAGCGTATCGGCTCTTTAGT 1929
Db 1755 AATCTTTACTGGAATAAACAGGATATGTCMAATCCTGAAGCTCGTCTCGCTAGT 1814
QY 1930 CCTAATAGCTTATGGAATGCAATTAATAGATATTTAGCTCTCTCAATTAATCTTATGGAGAC 1989
Db 1815 ACTCAATAGCTTTGGGATCCCTTTATAGATTTACGTTCTTATTCAAGATGCTTTGGAACG 1874
QY 1990 TGCAAACGAGGGTTCG---AGGAGACCGTCTTTTGGTGTGCTGGATATCTAATCT 2046
Db 1875 TAGTGTGTAGTATTTCTGAGACACGCTCGTGGTTGTGGGTCTCTGGAATTTGGGAACCT 1934
QY 2047 CTTCCATAAGCATAGTACAAAAACACACGCGGGTTTCGCCATTGAGTGGCGGTATGT 2106
Db 1935 CTTCCATAAGATCGGAATCTGTAATTCGAAATTCGAAATTCGCTCATATCAGTTCCGGATATGT 1994
QY 2107 CATAGGAGGAAACCTACATCTTGTTCAGATAGATTTCTTAGTCTGCATTTTGTACGT 2166
Db 1995 GTTAGGAGCCACAAATACTCGAGAGAGGATTTCTTTAGTGTGGCTTTCTGTCACTT 2054
QY 2167 CTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGTACATCTTACGGAGAAC 2226
Db 2055 ATTTGCAAAAGATAAAGACTACCTTTGTAAGCAAGACGCCGCAACGCTCTATGCGGGTTC 2114
QY 2227 TCTCTATTACAGCA-----CAACGAAACCTATCTCTCTCTTGGCAAACTACGGCC 2280
Db 2115 TGATATATACAGATGTGACGAGTTTGTATCTCACGGGTTATTTAATGGCCCTAA 2174
QY 2281 TTGTGCTGTTCTTATGTTCTCAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTA 2340
Db 2175 CACGTGTTGTTACGGGTTTCTAAAGAGATTCCTATTCTTTCTGGATGCACAAATTTACCTA 2234
QY 2341 CACCATACGATACAGTCTGAAACCAAGTATACACATATCTCTACTGTTTAAAGGAG 2400
Db 2235 TTGCCACACGGCCCAACATGACAACTGCTATACAGACTATCTCTGAAGTGAAGGTTTC 2294
QY 2401 CTGGGGAATCATAGTTTCTGTTTGTAGAAATTCGGTGAAGAGCTCCGATTTGCTTAGATGA 2460
Db 2295 TTGGGTAATGATACCTTGGGCTTAACTTTGTCTACTAGGTACTATCCGGTATTTAG 2354
QY 2461 AAGTCTCTATTTGAGCAGTACATGCGCTTCAATGAATTTGTCATGACATCA 2520
Db 2355 TTCTTCTATCTTTGATAGTATGACCGGTTTGCAAAATTAACAAGTTGTCTATGGCCACCA 2414

QY 2521 GGNAGCTTTTAAGAACACGGACAGAGCTCGTGAATTTGGAAGTAGCCGCTCTTGTGAA 2580
Db 2415 AGATGACTTTTAAAGAACCAACAAACAGAGCCGGGCTTTTGAAGCAGCGATCTTCTCAA 2474
QY 2581 TCTTGGCTTACCTATCGGATCCGATTGATAGGAATCAGACTGCCAAGATGCAACGTA 2640
Db 2475 CGTTTCTGTACCTATAGGTATATAAATTTGAGAACTCTCCTATGGAGAGAGTGTCTTA 2534
QY 2641 CAATCTAATCTTGTGTTTACTGTGGATCTTGTTCGTAGTAACCCGACTGTAGCAAC 2700
Db 2535 TGATCTTACACTGATGTATATACCTGATGTACCGCTCAATCCAAAGCTGTATGACAGG 2594
QY 2701 ACTGCGAATTTAGCGGTGATTTCTTGGAAAACTTTCGGTACGAAATTTGCAAGACAAAGCTTT 2760
Db 2595 ATTGGGATCAATGAGCTTTCCTGGTTAACACAGACTACGAATCTTGTAGACAGCTTT 2654
QY 2761 AGTCTTTCGTGACGGAAACCAATTTTTCCTTAACTCAAAATTTTGAAGCCTTTAGCCAAAT 2820
Db 2655 CATAGTTTCGCGGGTAACCATATTGCTTTAACTCTCTGGTGTGAGATGTTCACTCAGT 2714
QY 2821 TCTTTTGAATTCGCTGGGTCTCATCTCGCAATTAATAGACTTAGGAGCAAAATACCA 2880
Db 2715 TGTCTTGAATTAAGAGCTCTTCAAGAAATTTATAAGTAGATCTTGGCGCTAAGGTCCG 2774
QY 2881 ATTCTAA 2887
Db 2775 GTTCTAA 2781

RESULT 8

AAC81914
ID AAC81914 standard; DNA; 273254 BP.

XX AAC81914;

XX 15-SBP-2003 (revised)
DT 27-FEB-2001 (first entry)

XX Chlamydia pneumoniae genome DNA.

XX Genome; diagnosis; vaccine; ds.

XX Chlamydophila pneumoniae.

XX WC200027994-A2.

XX 18-MAY-2000.

XX 12-NOV-1999; 99WO-US026923.

XX 12-NOV-1998; 98US-0108279P.

XX 08-APR-1999; 99US-0128606P.

XX (REGC) UNIV CALIFORNIA.

XX Stephens R, Mitchell W, Kalman S, Davis R;

XX WPI; 2000-376516/32.

Isolated nucleic acid for use in diagnostic and analytical methods

encodes genomic sequence of Chlamydia pneumoniae.

Claim 2; Page 128-320; 320pp; English.

XX This invention describes a novel nucleic acid (N1) encoding a Chlamydia
XX pneumoniae protein (P1), given in the specification. The isolated nucleic
XX acid is useful for diagnostic and analytical methods, such as,
XX hybridization-based assays or amplification-based assays. The protein may
XX be used for diagnostic purposes, for their enzymatic or structural
XX activity, or as a vaccine. The invention also describes (1) a probe
XX comprising a hybridizing fragment of N1; (2) an isolated nucleic acid
XX (N2) that hybridizes under stringent conditions to N1; (3) an expression

CC cassette comprising N1 under the transcriptional regulation of a
CC transcriptional initiation region functional in an expression host, and a
CC transcriptional termination region; (4) a cell comprising an expression
CC cassette of (3) as part of an extrachromosomal element or integrated into
CC the genome of a host cell as a result of induction of the expression
CC cassette into the host cell, and the cellular progeny of the host cell;
CC (5) a method for producing a pl comprising growing a cell of (4) where
CC the protein is expressed and isolating the protein free of other proteins
CC ; (6) a purified polypeptide composition comprising at least 50 weight %
CC of pl; and (7) a monoclonal antibody binding specifically to the peptide
CC of (6). (Updated on 15-SEP-2003 to standardise OS field)

XX
SQ Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 U; 0 Other;
Query Match 17.7%; Score 531.2; DB 3; Length 273254;
Best Local Similarity 53.0%; Pred. No. 1.6e-135;
Matches 1415; Conservative 0; Mismatches 1183; Indels 74; Gaps 10;

QY 247 TCGTGAACCTACTCTCTAATTAAGGAAATGCACTCTAGAAAATATTCTCTGGAAACAGG 306
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 307 CACGCAATCAGAAAAGCTGTTTAAACAACACTAAGGCGGATTTCACATTTCACAGTTAA 366
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98408 --CAGCTTTAAGGAGGTTGTTTCTGACACTACGGAATCTTTAAGCTTTTGGCGGTAA 98465
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 367 CGGGAACCTCTATTGTTCCAAACGGTGGATGAGGAGCTGTAGCAGGGGCTGCTTTAA 426
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98466 GGGGTACTACCTTTCTTTTAAATTAAGTCTAGTGTGAGGCGGACACTTTCGT 98525
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 427 CAGCAGCGTGGTAGATAAATACCAACGTTTATAGGTTTCTTCGCTATCTTTTATGTC 486
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98526 TACAACCTGATAAAATCTGCTGCTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCC 98585
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 487 GTCTCTGGAAGTTGATTAACCTACCGGCAAGGCGGTAGTCTCTACGGGTAGCTT 546
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98586 ATCTCGGTAATCAACCCCTCAGGAAAAGTGCGATTAAATGTGGAGGGGATC--T 98642
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 547 GAGTTTGACAAAATGTGAGTTTGTCTCTTCAGCAAAAATCTTTCAACGGATAATGGCG 606
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98643 TACATTTGATAACAATGGAATCTTTTATTTAAACAGGATTAATGCTGAGGAAAATGGCG 98702
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 607 TCGTATCACCGCAAAATCTTTTCAATTAACAGGACTACAATGTGAGCTCTGTTTCTGA 666
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98703 AGCCATTTCTACCAAGATCTTTCTTTGAAAACAGCAGCGGATCGATTTCTTTTGAAG 98762
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 667 AATA-----CCTCCTCAAGAAAGCGGCGCATTCAGACTTCGGATGCCCTTAC 717
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98763 GAATTAATCGAGGCAACAGGAAAAGTGCGGCTATTTGTGCTACTGGTACTGTAGA 98822
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 718 CATTACTGGAACCAAGGGGAAGTCTCTTTTCTGACAAATCTTTCTCGGATTCTGGAGC 777
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98823 TATTACAAATAATACGGCTCTACCTCTCTCGAACAATATTGCTGAAGCTGCAGGTGG 98882
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 778 TCGAATTTTACAGAGCTCGGTGACTATTTCTTAATATGTAAGTTTCCCTTTATTGA 837
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98883 AGCTATAATAGCACAGGAAACTGTACAAATTAAGGGAATAGCTCTCTTGTATTTTCTGA 98942
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 838 CAATAAGGTACAGAGGCGAGCTCTCTCAACAAGCGGGGATATGTCAGGAGGTGCTATCTG 897
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98943 AATATGTGTAC---AGCGACCGAGGAAATGAGGAGCTCTTTCTGGAGATGCCG---- 98995
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 898 TGCCTTATAAACTAGTACAGATACTAAGGTACCCCTCACTGGAAATCAGATGTACTCTT 957
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 98996 -----ATGTTACCATATCTGGAATCAGAGTGTAATTT 99029
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 958 CAGCAACATACATCGAACACAGCGGAGGACTATCTATGTGAAAAGCTCGAATGCG 1017
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99030 CTCAGAAAACCAAGCTGTAGCTAATGCGGAGCCATTTATGCTAAGAACTTACACTGCG 99089
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1018 TTCCGGAGGACT-----TACCCTTATTCAGTAGAAATAGTGTCAATGGAGGTACAGTCTCT 1072
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99090 TTCCGGGGGGGGGGTATCTCTTTTCTACATATATAGTCCAAAGTACCACTGCAGGT 99149
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1073 AAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAATTCAGTTTATCCCGCATAGTGT 1132
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99150 AATGTTGGAGCCATTTCTATCTGCGCAGCTGGAGAGTGTAGTCTTTACAGAGACAGG 99209
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1133 GACATGTCTTTTGGGAATACAGTCACTTCTACTATCTCC---TGGGACGAATAGAAAT 1189
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99210 GACATTAACCTTCAATGGGAATGCCATTTGTGCAACTACACCAAACTACAAAAGAAAT 99269
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1190 AGTATCGACTTAGGACGAGTGCAGAGATGACAGCTTTGCGTTCGCTCTGCTAGAGCC 1249
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99270 TCTATTGACATAGGATCTACTGCAAGATCAGAAATTTACGTGCAATATCTGGCATAGC 99329
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1250 ATCTACTTCTATGATCCCATACTACAGGATCATCCACAACAGTTTACAGATGCTTTAAAA 1309
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99330 ATCTTTTCTACGATCCGATTTACTGCTAATACGGCTGCGGATTTACAGATATCTTTAAT 99389
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1310 GTTAATGAGACTCCGCGAGTCTGCACTACATATFACAGGGAACATCATCTTCACAGGA 1369
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99390 CTCAATAAGGCTGATGAGGTAATAGTACAGATTAATAGTGGGTGATTTGTTTCTGTT 99449
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1370 GAAAAGTTATCAGAGACAGAGCCGAGATTTCTAAAAATCTTTACTTTGGAAGCTACTACAG 1429
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99450 GAAAAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACAACCTCATTCTACGCTGAAGCAG 99509
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1430 CCTGTAACTCTTTTACAGGAGTACTCTATCTTTTAAAAACATGGAGTGACTCTGCAGACTCAG 1489
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99510 CCTGTAACTCTTAACTGCAGAAATTTAGTACTTTAAAGGTGGTGTCACTCTCGATACGAAA 99569
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1490 GAATTCACCTCAACAGCGAGATTTCTGCTCTGGAATAGGAGTGAAGAACTACTCTAGAAC- 1548
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99570 GCGTTTACTCAGACCGCGGTTCTCTGTTTATTTATGGATGCGGCGACAACTGTTAAAGCA 99629
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1549 ---TGCTGATCTAGCACCATAAACAATTTGGTCTTTAAATCAATCAGTTCTATAGACGTGCA 1606
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99630 AGTACAGAGAGGTCACTTTTAAACAGTCTTTCATTTCTGTAGACTTTTAGCGAGGTT 99689
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1607 AAGAAGGCAAAAATAGAACCAAAAGCTAGCTCAAAAATTTGACTTTTATCTGGAACCATC 1666
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99690 AAGAAGTTGTAATTTGCTTCTTCAGCAAGTAAATAATGTAGCCCTTAGTGTCCGAT 99749
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1667 ACTTTTATGGACCGACGCGGACGTTTATGAAATCATAGTTTAAAGAACTCTCAGTCC 1726
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99750 CTTCTTTTGGATAACCAAGGGAATGCTTATGAAATCAGCACTTAGGAAAATCTCAAGAC 99809
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1727 TAGGACATCTTAGACTCAAAAGCTCTTGAACTGTAAACAAGCAGCAGTGACTCCAGAT 1786
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99810 TTTTTCATTTGTCAGCTCTCTCTCTGGTACTGCAACAACTACAGATGTTCCAGCGTT 99869
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1787 CTTAATATGGGTGAGAAATTCATTTACGGCTATCAGGGAATCTTGGGCCCAATTTGTTGG 1846
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99870 CTTACAGTAGCAACTCTACGCACTATGGGTATCAAGGTACTTTGGGAATGACTTGGGTT 99929
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1847 G-----GACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAATAACTGCG 1894
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99930 GATGATACCGCAAGCACTCCAAAGACTAAGACAGCGACATTAAGCTTGGCAATACAGCG 99989
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1895 TATATTCTTAATCCCGAGGATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTT 1954
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 99990 TACCTTCGAATCTTGAGGCTCAAGGACCTTTAGTTCTTATAGCTTTGGGGAATCTTTT 100049
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 1955 ATGATATTAGTCTCTCCATTTATTTATGGAGACTGCAAAAGAGGTTGCGGGAGAC 2014
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 100050 TCAGATCCCAAGCAATCAAGGTGTCATAGAGAGAAGTGTCTTGACTCTTTGTTTCAGAT 100109
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 2015 CGTGTCTTTTGTGTGCTGATTTACTTCTTCCATAAGGATAGTACAAAACACCA 2074
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 100110 CGAGGCTCTCGGCTGCGGAGTGCCTCAATTTCTTAGATAAAGATAAGAAAGGGGAAAAA 100169
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 2075 CCGCGGTTTTCGCAATTTGAGTGGCGGTTATGTATAGGAGGAAAACTACATATCTTTCA 2134
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 100170 CCAAAATACCGTCATAAATCTGTTGATATGCTATCGGAGGTGACGCGCAAACTTGTCT 100229
DB TACTGGAATAGACTATCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGGATTCCG- 98407

QY 607 TCGTATACCGCAAAACTCTTTTCAATAACAGGACTACAATGTCAAGTCTGTGTTTCTGA 666
Db 510 AGCCATTTCTACCAAGAACTTTCTTTGAAAAACAGCAGGGATCGATTTCTTTTGAAGG 569
QY 667 AATA-----CCTCCTCAAGAAAGCGGAGCCATTACAGACTTCGATGCCCTTAC 717
Db 570 GAATTAATCGAGCGCAACAGGAAAAAGGTGGGCTATTGTGCTACTGTAGTA 629
QY 718 CATTACTGAAACCAAGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGATTCTGGAGC 777
Db 630 TATTACAAATAATACGGCTCTTACCCTCTTCTCGAACATAATGCTGAAGCTGCAGGTGG 689
QY 778 TCGAATTTTACAGAGCCTCGGTGACTATTCTTAATAATGCTAAAGTTTCTTTATGCA 837
Db 690 AGCTATAAATAGCACAGGAAACTGTACAATAACAGGGAATAGCTCTCTTGTATTTTCTGA 749
QY 838 CAATAAGGTACAGAGGAGCAGTCTCTCAACAACGGGGGATATCTCAGAGAGGTGCTATCTG 897
Db 750 AATAGTGTAC---AGCGCCGAGGAATGGAGAGCTCTTTCTGGAGATGCCG----802
QY 898 TCGTTATAAACTAGTACAGATACTAAGGTCACTTCACTGGAATACAGATGTTACTCTT 957
Db 803 -----ATGTTACCATATCTGGGAATCAGAGTGAACTTT 836
QY 958 CAGCACANTATACATCGACAACAGCGGAGAGCTATCTATGTGAAAAAGCTCGAATGBC 1017
Db 837 CTCAGAAACCAAGCTGTAGCTTAATGGCGGAGCCATTTATGCTAAGAAGCTTTACACTGCC 896
QY 1018 TTCCGAGAGACT-----TACCCTATTAGTAGAATAAGTCAATGGAGGTACAGCTCC 1071
Db 897 TTCCGGGGGGGGGGGTATCTCCTTTTCTAACATAATAGTCCAAAGGTACCACTGTCAGG 956
QY 1072 TAAAGTGGAGCCATAGCTATCGAAGATAGTGGGAATTTAGTTTATCGCGGATAGTGG 1131
Db 957 TAAAGTGGAGCCATTTCTATCTGCGAGCTGAGAGTGTAGTCTTTTACAGAGAAGCAGG 1016
QY 1132 TGACATTTCTTTTAGGAAATACAGTCACTTCTACTACTCC---TGGAGCAANTAGAG 1188
Db 1017 GGACATTTACTCAATGGGAATGCCATTTGTCACACTACACCAAACTACAAAAAGAA 1076
QY 1189 TAGTATCGACTTAGAAACAGGTGCAAGATGACAGCTTTGCGTTCTGCTGGTAGAGC 1248
Db 1077 TTTCTATTGACATAGATCTACTGCAAGATCAGGATTTACGTGCAATATCTGGGCATAG 1136
QY 1249 CATCTACTTTTAATGCCAATAACTACAGGATCATCCACAACAGATTACAGATGTCTTAA 1308
Db 1137 CATCTTTTCTACGATCCGATTACTGCTAATACGGCTGCGGATTTCTACAGATACTTAA 1196
QY 1309 AGTTAATGAGCTCCGGCAGATTCTGCACTACAATATACAGGAACATCATCTTACAGG 1368
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QY 1369 AGAAAGTTATCAGAGACAGGCGCGAGATTCTAAAAATCTTACTTCAAGCTACTACA 1428
Db 1257 TGAAAGCTCTGAGATGAGCAAAAGTTGCAACACCTCACTTTCTACGCTGAGCA 1316
QY 1429 GCCTGTAATCTTTTACAGAGGTACTCTATCTTTTAAACATGAGGTGACTCTCAGACTCA 1488
Db 1317 GCCTGTAATCTTAACTGCAAGGAAATTTAGTACTTAAAGCTGGTGCATCTCGATACGAA 1376
QY 1489 GCAATTTCAACAGGAGATTCTGCTCGAATGAGAGTGGAGTCACTCTAGAAC 1548
Db 1377 AGGCTTTACTCAGCCGGGTTCTCTGTTAATGATGGGCAACAGTTTAAAGC 1436
QY 1549 ---TGCTGATACAGCACAATAAAATTTGGTCAATTAACATCACTTCTATAGACGGTGC 1605
Db 1437 AAGTACAGAGGAGTCACTTTTAAAGGCTTTCCATTTCTGTAGACTCTTTAGGCGAGG 1496
QY 1606 AAGAAGGCAAAATAGAAACCAAGCTACGTCAAAAATCTGACTTTATCTGGAACCAT 1665
Db 1497 TAAGAAAGTGTAAATGTCTGCTCTGAGCAAGTAAATAATGAGCCCTTAGTGGTCCGAT 1556
QY 1666 CACTTTATTGGACCGCAGCGGACAGTTTTATGAAATCATAGTTTAAAGAAATCCTCAGTC 1725

Db 1557 TCTTCTTTTGGATAACCAAGGAATGCTTTATGAAATCAGACTTAGGAAAAACTCAAGA 1616
QY 1726 CTACGACATCTTAGAGCTCAAAAGCTTCTGGAAGTGTAAACAAGCACCAGCTGACTCCAGA 1785
Db 1617 CTTTTCATTTGTGCACTCTCTGCTCTGGGTATCTGCAACAACCTACAGATGTTTCCACGGT 1676
QY 1786 TCTATAATGGGTGAGNAATTCATTTACGGCTATCAGGAACTTTGGGGCCCAATTTGTTG 1845
Db 1677 TCTACAGTAGCAACTCTCTACGCACTATGGGTATCAAGGTACTTGGGGAATGACTTGGGT 1736
QY 1846 GG-----GGAACAGGGGGCTTCTACGACTGCAACCTTCAACTGCACTPAAACTGG 1893
Db 1737 TGATGATACCGCAAGCACTTCCAAAGACTAAGACAGCGACATTAGCTTGGACCAATACAGG 1796
QY 1894 CTATATCTCTAATCCGAGGCTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATT 1953
Db 1797 CTACCTTCCGAATCTGAGCGTCAAGGACCTTTAGTTCTTAATAGCTTTGGGGATCTTT 1856
QY 1954 TATAGATATTAGCTCTCTCCATTATCTTATGAGAGCTGCAAAACGAAGGGTTGCAGGGAGA 2013
Db 1857 TTCAGACATCCAAAGCAATTCAAGGTGTCTATAGAGAGAAGTGTCTTGACTTTTGTTCAGA 1916
QY 2014 CCGTCTTTTGGTGTCTGGATTATCTAACTTTCTTCCATAAGGATAGTACAAAAACAG 2073
Db 1917 TCGAGGCTTCTGGGCTCGGGAGTCGCCAATTTCTTAGATAAAGATAAGAAAGGGGAAAA 1976
QY 2074 AGCGGGTTTCCCATTTTGGTGGGTTATCTCTATAGAGGAAACCTACATACTTGTTC 2133
Db 1977 AGCGAATACCGTCTAATAATCTGGTGGATGCTATCGAGGTGAGCGGCAAACTTGTTC 2036
QY 2134 AGATAAGATTCTTAGTGTGCAATTTTGTGAGCTCTTTTGAAGAGATAGAGACTTTGT 2193
Db 2037 TGAAAACTTAAATTAGCTTTGCTTTTGCCTTTTGCCTTTTGGTATGCGATAAAGATTCTTAGT 2096
QY 2194 AGCTAAGATCAAGGTACAGTCTACGGAGGAATCTCTATATACCGAGCAACAGAAACCTA 2253
Db 2097 CGCTAAAAATCATACTGATACCTATGCGAGGACCTTCTATATCCAACACATTTACGAATG 2156
QY 2254 TATCTCTCTCTTCCAAACTACGGCTTTGTCGTTGCTTATGTTTCTTACAGAGATCC 2313
Db 2157 TAGTGGGTTTATAGTTGTCTCTTAGATAAA---CTTCTGGCTCTTGGAGTCTAFAACC 2213
QY 2314 TGTCTCTTTTTCAGGAACTTTAGCTACACCCATACGGATACAGTACTGAAACCAAGTA 2373
Db 2214 CCTCGTTTTAGAAAGGCGAGCTCGCTTATAGCCACGCTCAGTATGATCTGAAGACAAAGTA 2273
QY 2374 TACAACATATCTTACTGTTTAAAGGAAGCTGGGGAATGATAGTTTTCGCTTTTGAATTCGG 2433
Db 2274 TACTCGGTATCCTGAGGTGAAAGGTTCTTGGGGGAATAATGCTTTTAAACATGATGTGGG 2333
QY 2434 TGGAAGAGCTCCGATTTGCTTAGATGAAAGTCTCTATTTGAGAGTACATGCCCTCAT 2493
Db 2334 AGCTTTCTCTATCTTCTTCTTCTGATACCTGCAATGTTTGTATCTATGCTTCAACTAT 2393
QY 2494 GAAATTCAGTTTGTCTATGACATCAGGAAAGTTTAAAGAACAGGGAACAGAGCTCG 2553
Db 2394 CAAACTGAATCTGACCTATATACGTCAGGACAGCTTCTCGGAGAAAGGTACAGAAAGGAG 2453
QY 2554 TGAATTTGGAAGTAGCCGCTCTGTGAAATCTTGCCTTACTATCGGATCCGATTTGATAA 2613
Db 2454 ATCTTTTATGACAGCAACCTCTTCAATTTATCTTTGCTTATAGGGGTGAAGTTTGAGAA 2513
QY 2614 GGAATCAGACTGCCAAGATGCAACGTCAATCTAATCTTGGTTATATCTGTGATCTTGT 2673
Db 2514 GTTCTCTGATGTAATGACTTTCTTATGATCTGACTTATCCATGTTTCTGATCTTAT 2573
QY 2674 TCGTAGTAACCCCGACTGTACAGCAACACTGCGAANTAGCGGTGATTTTGAACACCTT 2733
Db 2574 CCGAATGATCCCAATGCATCTACAGCACTTGTATCAGCGAGGCTCTTTGGGAAACTTGA 2633
QY 2734 CGGTACGAATTTGGCAAGCAAGCTTTAGTCTCTGTCAGGGAACCAATTTTGTCTTTAA 2793

Db 2634 TGCCATAACTAGTACACGACGAGCCCTTGCAAGTGGTGCAGGAGTCACTACGCGCTTCTC 2693
 Qy 2794 CTCAATTTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGGTGCATCTCGCANTTA 2853
 Db 2694 TCCTATGTTTGAAGTGTCTCGGCCAGTTTGTCTTTGAAGTTCTGTGATCCTCAAGGATTA 2753
 Qy 2854 CAATGTAGCTTAGGAGCAAAATACCAATTTCTA 2886
 Db 2754 TAATGTAGATCTGGGGGTAAGTCCAAATTTCTA 2786

RESULT 10

ABL91231
 ID ABL91231 standard; DNA; 2787 BP.

XX ABL91231;

XX 29-AUG-2003 (revised)

DT 29-JUL-2002 (first entry)

XX Chlamydia pneumoniae cp0010 ORF DNA, SEQ ID NO:96.

XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CWL029; open reading frame; ORF; gene; ds.

XX Chlamydoiphila pneumoniae.

XX Key Location/Qualifiers

XX CDS 1..2787

XX /*tag= a

XX /product= "cp0010"

XX sig_peptide 1..75

XX /*tag= b

XX mat_peptide 76..2784

XX /*tag= c

XX /product= "Mature protein"

XX W0200202606-A2.

XX 10-JAN-2002.

XX 03-JUL-2001; 2001WO-IB001445.

XX 03-JUL-2000; 2000GB-00016363.

XX 11-JUL-2000; 2000GB-00017047.

XX 21-JUL-2000; 2000GB-00017983.

XX 07-AUG-2000; 2000GB-00019368.

XX 18-AUG-2000; 2000GB-00020440.

XX 14-SEP-2000; 2000GB-00022583.

XX 10-NOV-2000; 2000GB-00027549.

XX 22-DEC-2000; 2000GB-00031706.

XX (CHIR-) CHIRON SPA.

XX Ratti G, Grandi G;

XX WPI; 2002-154726/20.

XX N-PSDB; ABB90573.

XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.

XX Claim 5; Page 88-89; 364pp; English.

XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is

CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)

XX
 SQ Sequence 2787 BP; 785 A; 568 C; 619 G; 815 T; 0 U; 0 Other;

Query Match 17.6%; Score 527; DB 6; Length 2787;

Best Local Similarity 52.9%; Pred. No. 2.5e-135;

Matches 1413; Conservative 0; Mismatches 1185; Indels 75; Gaps 10;

Qy 247 TGCTGGAACCTACCTACCTATTTAAGGGAAATGTCACCTCTAGAAAATATTCCTGSAACAGG 306

Db 156 TATGGAAATAGACTATCTCTGACGAGATATACTCTGCAAAACCTTGGGATTCGG- 214

Qy 307 CACAGCAATCACAAAAGCTGTTTAAACAACACTAAGGGCGATTGACTTTTCACAGTAA 366

Db 215 --CAGCTTTAAACGAAGGTTGTTTCTGACACTACGGAATCTTTAAGCTTTGCCGTAA 272

Qy 367 CGGGAACCTCTATTGTTCCAAACGGTGGATGACGAGGACTGTACGAGGGGCTGCTGTAA 426

Db 273 GGGGTACTCACTTTCTTTTAAATATTAAGTCTAGTCTGAAGGCGCAGCACTTCTGT 332

Qy 427 CACGAGCGTGTAGATAAATCTACACGTTTATAGGGTTTCTTCGCTATCTTTTATTGC 486

Db 333 TACAACCTGATAAAATCTGCTGTAACAGGATTTTCAGTCTTACTTTCTTAGCGGCCCC 392

Qy 487 GTCTCTCTGGAAGTTTCGATAACTACCGGCAAGGAGCGCTTAGCTGCTCTACGGGTAGCT 546

Db 393 ATCATCGGTAATCACAAACCCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGATC--T 449

Qy 547 GAGTTTGACAAAATGTGAGTTGCTCTTCAGCAAAAACCTTTTCAACGGAATATGCGG 606

Db 450 TACATTTGATAACAATGGAACTATTTTATTTAAACAAGATTACTGTGAGGAAAATGCGG 509

Qy 607 TGCTATCACCGCAAAAACCTCTTTCAATTAACAGGAGCTACAAATGTCACTCTGTTTTCTGA 666

Db 510 AGCAATTTCTACCAAGNAATCTTTCTTTGAAAACACAGCACGGGATCGATTCTTTTGAAG 569

Qy 667 AAATA-----CCTCTCAAGAAAGCGGAGCCATTTCAGACTTCCGATGCCCTTAC 717

Db 570 GAATAAATCGAGCGCAACAGGGAATAAGGTGGGCTATTTTGTCTACTGGTACTGTAGA 629

Qy 718 CATTAATGGAACCAAGGGGAAGTCTCTTTTCTGCAAACTCTTCTCGGATTCGGAGC 777

Db 630 TATTACAAATAATACCGGCTCTACCCCTCTTCTCGAACAATATTGCTGAAGCTGCAGTGG 689

Qy 778 TGCAATTTTACAGAGCCTCGGTGACTATTTCUATAATGCTAAAGCTTTCCTTTATTGA 837

Db 690 AGCTATAAATAGCACAGGAAACTGTACAATTACAGGAATACGCTCTCTGTATTCTGA 749

Qy 838 CAATAAGGTTCACAGGAGCGAGCTCCTCAACAACCGGGGATATGTTCAGAGGATGCTATCTG 897

Db 750 AAATAGTGTGAC---AGCGACCGCAGGAAATGGAGGAGCTCTTTCTGGAGATGCCG--- 802

Qy 898 TGCTTATAAACTAGTACAGATACAGTACAGGTCACCTCAGTGGAAATCAGATGTACTCTT 957

Db 803 -----ATGTTACCATACTCTGGAATCAGAGTGTAACTTT 836

Qy 958 CAGCAACAATACATCGACAACAGCGGAGGAGCTATCTATGTGAAAAGCTCGAAGCTGC 1017

Db 837 CTGAGGAACCAAGCTGTAGCTTAATGCGGAGCCATTTATGCTTAAGAACTTACACTGGC 896

Qy 1018 TTCCGGAGGAC-----TTACCCCTATTTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCC 1071

Db 897 TTCCGGGGGGGGGGGATCTCTCTTTTAAACAATAATAGTCCAAAGGTACCACTGCAGG 956
QY 1072 TAAAGGTGAGCATAGCTATCGAAGATAGTGGGAAATTGAGTTATTCGCCGCGATAGTGG 1131
Db 957 TAAAGGTGAGCAATCTCTATCTGCGAGCTGGAGAGTGTAGTCTTTTACAGCAGACGAG 1016
QY 1132 TGACATGTCTTTTGGAGAAATACAGTCACTTCTACTACTCC---TGGAGCGAATAGAAG 1188
Db 1017 GGACATATACCTTCAATGGGAATGCCATTTGTCACTACACCAAACTACAAAAGAAA 1076
QY 1189 TAGTATCGACTTAGGAACAGAGTGAAGATGACAGCTTTGCGTTCTGCTGGTGTAGAGC 1248
Db 1077 TTCTATGTACATAGGATCTCTGCAAAAGATCAGAAATTTACGTGCAATATCTGGGCATAG 1136
QY 1249 CATCTACTTCTATGATCCCAATACCTACAGGATCATCCAAACAGATTACAGATGTCTTAAA 1308
Db 1137 CATCTTTTCTACGATCCGATTAATCTGCTAATACGGCTGCGGATCTTACAGATCTTAAA 1196
QY 1309 AGTTAATGAGCTCCGGGAGATTTCTGCACTACAAATACAGGAACATCATCTTCCACAGG 1368
Db 1197 TCTCAATAAGGCTGATGCGAGGTAATAGTACAGATTATAGTGGGTGCAITTTGTTTCTGG 1256
QY 1369 AGAAAGTTATCAGACACAGAGCGCCAGATTCTAAAAATCTTACTTTGGAAGCTACTACA 1428
Db 1257 TGAAGAAGCTCTGGAAGTGAAGCAAAAGTTGAGACAACTCTACTTACGCTGAGCA 1316
QY 1429 GCGTGAATCTTTTACGAGGTACTCTATCTTTTAAACATGAGGAGTCACTCTGAGACTCA 1488
Db 1317 GCGTGAATCTTAACTGACAGGAAATTTAGTACTTAAACGTGGTGTCACTCTCGATACGAA 1376
QY 1489 GGCATTCATCAACAGGAGATTTCTGCTCGAAATGGAGCTAGGAATCACTCTAGAAC 1548
Db 1377 AGCGTTTACTCAGACCGCGGTTCTCTGTATTATGAGTGGGCAACAGCTTAAAGC 1436
QY 1549 ---TGCTGATACTAGCACCAATAAATTTGGTCAATTAACATCAGTCTTATAGACGGTGC 1605
Db 1437 AAGTACAGAGGAGTCACTTTAAAGGCTTTTCCATTTCTGTAGACTCTTTAGGCGAGG 1496
QY 1606 AAGAAGGCAAAATAGAAACCAAGACTACGTCAGAAATCTGACTTTTATCTGGAACCAT 1665
Db 1497 TAAGAAAGTTGAATTTGCTTCTGACAGCAAGTAAATATGAGCCCTTAGTGTCCGAT 1556
QY 1666 CACTTTATTTGGACCGGACCGGCTTTTATGAAATCATAGTTTAAAGAAATCTCAGTC 1725
Db 1557 TCTTCTTTTGGATAACCAAGGGAATGCTTATGAAATCAGACTTAGGAAATACTCAAGA 1616
QY 1726 CTACGACATCTTAGAGCTCAAAAGCTTCTGGAATGTAACAAGCACGCGAGTCACTCCAGA 1785
Db 1617 CTTTTCATTTGTGACGCTCTCTGCTCTGGGTACTGCAACAACTACAGATGTTCCAGCGT 1676
QY 1786 TCTATAATGGGTGAGAAATTCATTTACGGCTATCAGGAACTTGGGGCCCAATTTGTTG 1845
Db 1677 TCTACAGTAGCAACTCTCTACGCACTATGGGTATCAAGGTACTTGGGGAATGACTTGGGT 1736
QY 1846 GG-----GGACAGGGGCTTACGAGTGCACCTTCACTGGAGCTAAACTCG 1893
Db 1737 TGATGATACCGCAAGCACTCCAAAGACTAAGACAGCGACATAGCTTGGACCAATACAGG 1796
QY 1894 CTATATTCCTAATCCCGAGGATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTT 1953
Db 1797 CTACCTTCGGAATCTCTGAGGCTCAAGGACCTTTAGTTCCTAATAGCTTTGGGATCTTT 1856
QY 1954 TATAGATATAGCTCTCTCCATTAATTTATGAGACTGCAAAAGAGGGTTGAGGGAGA 2013
Db 1857 TTCAAGACATCCAGCGATTAAGGTGTCTATAGAGAAAGTGTCTTTCAGCTCTTTGTTCAGA 1916
QY 2014 CCGTGTCTTTTGGTGTGGATATCTAATCTTCCATAGGATAGTACAAAAACAGC 2073
Db 1917 TCAGGCTTCTGGGCTGCGGAGTCTCGCAATTTCTTAGATAAGATAAGAAAGGGGAAA 1976
QY 2074 ACGCGGTTTTCGCCATTTGAGTGGCGGTTATGTCTATAGGAGGAAACCTACATCTTTGTTTC 2133
Db 1977 ACGCAATACCGTCAATAATCTGGTGGATATGCTATCGGAGGTGCGCGCAACTTTGTTTC 2036

QY 2134 AGATAAGATCTTAGTGTGTCATTTTGTGTCAGTCTTTTGAAGAGATAGAGACTACTTTGT 2193
Db 2037 TGAATACTTAATAGTCTTTGCTTTTCCAACTCTTTGGTAGCGATAAAGATTCTTAGT 2096
QY 2194 AGCTAAGATCAAGGTACAGTCTACGGAGGAATCTCTATTACCAGCAACAGAAACCTA 2253
Db 2097 CCCTAAAATCATACTGATACCTATGACAGGACCTTCTATATCCAAACATTCAGAAATG 2156
QY 2254 TATCTCTCTCTTCCCTGCAAACTACGGCTTTGTTGTGTTCTTATGTTTCTTACAGATTC 2313
Db 2157 TAGTGGGTTCAATAGTGTGTTCTTAGATAAA---CTTCTGCTCTTGGAGTCATAAAC 2213
QY 2314 TGTCTCTTTTTCAGAAACCTTAGCTACACCATACGGATTAACGATCTCGAAACCAAGTA 2373
Db 2214 CCTCGTTTATAGAGGCGAGCTCGCTTATAGCCACGTCAGTAATGATCTCAGAGCAAGTA 2273
QY 2374 TACAACATATCTACTGTTTAAAGGAGCTGGGGGAATGATAGTTTTCGCTTTAGAAATCG 2433
Db 2274 TACTCGTATCTGAGGTGAAAGGTTCTTTGGGGGAATAATGCTTTTAAATGATGTTGG 2333
QY 2434 TGAAGAGCTCCGATTTGCTTAGATGAAGTGTCTTATTTGAGCAGTACATGCCCCTTCA 2493
Db 2334 AGCTTCTCTCATCTTATCTCTGAATACCTGCAATGTTTGTATACCTATGCTCCATAC 2393
QY 2494 GAAATTCGATTTGCTATGCAATCAGGAAGGTTTAAAGAACAGGGAACAGAGCTCG 2553
Db 2394 CAAACTGATCTGACCTATATATACGTACAGGACAGCTTCTCGAGAAAGGTACAGAAAG 2453
QY 2554 TGAATTTGAAGTAGCGCTTTGTAATCTTGCCTTACCTATCGGATCCGATTTGATAA 2613
Db 2454 ATCTTTTGTAGCAGCAACCTCTTCAATTTATCTTTGCTATAGGGGTGAAGTTGAGAA 2513
QY 2614 GGAATCAGACTGCCAAGATGCAACGTACAATCTTCTGTTATCTGATCTGATCTTGT 2673
Db 2514 GTTCTCTGATTTGATGACTTTTCTATGATCTGACTTATCTATGTTTCTGATCTTAT 2573
QY 2674 TCGTAGTAACCCGAGTGTACGACAACTGCGAATAGCGGTGATCTTGGAAACCTT 2733
Db 2574 CGCAATGATCCCAATGCACTTACAGCACTTGTAAATCAGCGGAGCTCTTGGAAACTTA 2633
QY 2734 CGGTACGAATTTGGCAAGCAAGCTTTAGTCTCTGTCAGGGAACCATTTTGTCTTTAA 2793
Db 2634 TGCCATAATCTTAGCAGCAGCGCTTGAAGTGTGCGAGCAGTCACTACGCTTCTC 2693
QY 2794 CTCAAATTTGAAGCTTTAGCCAAATTTCTTTTGAATTCGTTGGGTCACTCGCAATTA 2853
Db 2694 TCTATGTTTGAAGTGTCTCGCCAGTTTGTCTTTGAAGTTCTGATCTCTACGGATTTA 2753
QY 2854 CAATGTAGCTTAGGAGCAAAATACCAATTTCTA 2886
Db 2754 TAATGTAGTCTTGGGGTAAAGTTCCAATTTCTA 2786

RESULT 11

AAZ61509

ID AAZ61509 standard; DNA; 2957 BP.

XX

AAZ61509;

AC AC (revised)

DT 15-SEP-2003 (first entry)

DT 19-JUN-2000

XX

XX DNA encoding the CPN100395 polypeptide.

XX

XX CPN100395; Chlamydia infection; immune response; vaccine; ss.

XX

XX Chlamydia pneumoniae.

OS

XX Key Location/Qualifiers

FH 101..2857

FT CDS /tag= a

XX

PN	WO200011183-A2.
XX	
FD	02-MAR-2000.
XX	
PF	18-AUG-1999; 99WO-IB001449.
XX	
PR	20-AUG-1998; 98US-0097187P.
PR	20-AUG-1998; 98US-0097188P.
PR	20-AUG-1998; 98US-0097189P.
PR	20-AUG-1998; 98US-0097190P.
PR	20-AUG-1998; 98US-0097195P.
PR	20-AUG-1998; 98US-0097196P.
PR	20-AUG-1998; 98US-0097197P.
PR	27-AUG-1998; 98US-0097191P.
PR	17-AUG-1999; 99US-00376770.
XX	
PA	(CONN-) CONNAUGHT LAB LTD.
XX	
PI	Murdin AD, Oomen RP;
XX	
DR	WPI; 2000-224703/19.
DR	P-PSDB; RAY69369.
XX	
PT	Novel antigens and corresponding DNA molecules that can be used to
PT	prevent, treat and diagnose disease caused by Chlamydia infection in
PT	mammals, especially humans.
XX	
CC	Claim 1; Fig 15-E; 201pp; English.
XX	
CC	AZ61502-09 encode Chlamydia pneumoniae polypeptides. The polypeptides
CC	are present in the bacterial membrane structure, in the external vicinity
CC	of the membrane structure, in the inclusion membrane structure, in the
CC	external vicinity of the inclusion membrane structure, and in the
CC	cytoplasm of the infected cell. The polypeptides may be used to prevent,
CC	treat and detect the presence of Chlamydia infection and/or the presence
CC	of Chlamydia in a sample. The polypeptides may also be used to induce an
CC	immune response in a mammal. The vaccine vector comprising the
CC	polynucleotides is used to induce an immune response in a mammal.
CC	Antibodies directed against the polypeptides may also be used
CC	therapeutically to treat and/or prevent a Chlamydia infection. (Updated
CC	on 15-SEP-2003 to standardise OS field)
XX	
SQ	Sequence 2957 BP; 818 A; 598 C; 683 G; 858 T; 0 U; 0 Other;
	Query Match 17.5%; Score 524.6; DB 3; Length 2957;
	Best Local Similarity 53.4%; Pred. No. 1.2e-134;
	Matches 1424; Conservative 0; Mismatches 1159; Indels 84; Gaps 12;
QY	242 GAAGATGCTGGAACTACTACCTATTTAAGGGAATGTCACTAGAAAAATATTCCTGGA 301
Dd	260 GATGCTAGTGGCAGACCTATTTCTCGATGGGATGTCTCGATA---AGCCAAGCAGG 316
QY	302 ACAGGCACACGAATCACAAAAGCTGTTTAAACAACATAAGGCGAATTGACITTCACA 361
Dd	317 AAACAACGAGCTTAACCAAGTGTTTTTCTAACACTCGAGGAATCTTACCCTCTTA 376
QY	362 GGTAACGGGAACCTCTTATTGTTCCAAACGGTGGATCAGGCACTGTAGCAGGGGCTGCT 421
Dd	377 GCGAACGGATTTCTCTCATTTTGGACAATATATTTTCGTCTACTGTTGAGGTGTGTT 436
QY	422 GTTAAACGACGGTGGTAGATAAATCTACACGTTTATAGGGTTTCTTCGTATCTTTT 481
Dd	437 GTTAGCAATACAGCAGCTTCTGGGATACGAAATTTCTCAGATTTTCAAATCTTCGGATG 496
QY	482 ATTGCGTCTCTGGAAGTTCGATAACTACCGGCAAGGCGGTAGCTGCTCTACGGGT 541
Dd	497 CTTCGAGCTCT-----AGACCACAGGTAAGGAGGCCATTAAAAATTACCGATGGT 547
QY	542 AGCTTGAGTTTGACAAAAATGTTCAGTTTTCGTCTTTCAGCAAAAATTTTCAACGGATAAT 601
Dd	548 --CTGGTGTGTTGAGAGTATAGGAACTCTGATCTTT--AATGAAATAGCTCTAGTGAANAAT 604
QY	602 GCGGGTCTATACCGCAAAAATCTTTCTATTAAACAGGGACTACAATGTCAGCTCTGTTT 661

Db 1655 GTAGATGCTCAGGGAACTATTATGAGCATCATTAATCTCAGTCAACAGCAGGCTCTTTCCT 1714
Qy 1733 ATCTTAGAGCTCAAGCTTCTGGAACTCTACAGACCGCAGTCACTCCAGATCCCTATA 1792
Db 1715 TTAATAGAGCTTCTGCAAGAGAACGATGACTACTACAGATATCCCCGATACCCCAATT 1774
Qy 1793 ATGGGTGAGAAATTCATATAGGCTATCAGGAACTTGG-----GGCCCAATTGTTTGG 1846
Db 1775 CTAATATACGATACATCATGATGGGTATCAAGGAACTGGAATATGTTTGGTGCAGAT 1834
Qy 1847 GGGACAGGGCTTTACAGCTCAACCTTCAACTGGAATAAACTGGCTATATTCCTAAT 1906
Db 1835 GCAACTGCAAAAACAAAAATGCTACCTTAACTTGGACTTAAACAGGATACAAGCCGAAT 1894
Qy 1907 CCCAGCGTATCGCTCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGC 1966
Db 1895 CCAGAACGTAGGGACCTTGGTCTCTAATAGCCTGTGGGGTCTTTTGTGATGATCCGC 1954
Qy 1967 TCTCTCCATTATCTATGAGACTGCAACGAAGGGTTGCGAGGAGCCGTGCTTTTGG 2026
Db 1955 TCCATTAGAGCTCATGACCGGAGCACAGTTCGTTATCTTCGTCAACAAATTTGG 2014
Qy 2027 TGTGCTGATATCTAACTTTCTTCATAGGATAGTACAAACACAGACGGGTTTGC 2086
Db 2015 GTATCAGGAATCGCGACTTTTGTGATGAAGATCAGAAAGGAAACCAACGTAGTTATCGT 2074
Qy 2087 CATTTGAGTGGCGTTATGCTAGAGGAAACCTACATCTTGTTCAGATAAGATCTT 2146
Db 2075 CATTTAGCGGGTTATGCATTAGGAGGAGTCTTCACGGCTTCTGAAATTTCTTT 2134
Qy 2147 AGTGTGCTATTTGTGAGCTTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAACTAA 2206
Db 2135 AATTTTGTCTTTTGTGAGCTTTTGGCTACGACAGGACCATCTTGTGGCTAAGAACCAT 2194
Qy 2207 GGTACAGTCTAGGAGGAATCTCTATACAGACCAACGAACCTATATCTCTCTCT 2266
Db 2195 ACCCATGTATATGACGGGCAATGAGTTACCGACACCTCGGAGAGTCAAGACCCCTCGT 2254
Qy 2267 TGCMAACTAGCGCTTTGTTGCTTATGTTCTTACAGAGATCTCTGTTCTCTTTTCA 2326
Db 2255 AGAT-----TTTGTGAGGAATCTGACCTCCCTACCTTTTGTCTCAAT 2299
Qy 2327 GGAACCTTTAGCTACACCATAGGATAACGATCTGAAACCAAGTATACACATATCT 2386
Db 2300 GCTCGTGTGCTTTATGGCCATACCGACATAACATGACCAAAAGTACACTGGCTATTCT 2359
Qy 2387 ACTGTTAAAGAGCTGGGGGATGATGTTTGGCTTTAGAAATTCGTTGAGAGAGCTCG 2446
Db 2360 CCTGTTAAGGGAAGCTGGGGAAATGATGCTTCCGTATAGATGTGGAGGAGCTATCCCG 2419
Qy 2447 A---TTTGCTTAGATCAAAAGTGTCTATTGTGAGCAGTACATGCCCTTCATGAAATTCGAG 2503
Db 2420 GTAGTTGCTTACGAGCTCGGCTTGGTGGATACCCACAGCCATTTCTAAACCTAGAG 2479
Qy 2504 TTTGCTATGCACATCAGGAAGGTTTAAAGACAGGGAACAGAGCTCGTGAATTTGGA 2563
Db 2480 ATGATCTATGCACATCAGAATGACTTTAGGAAACCGCACAGAGGCCCTTCTTTCCCA 2539
Qy 2564 AGTAGCGGCTTGTGAATCTTGCCTTACCTATCGGATCCGATTCGATAGGAATCAGAC 2623
Db 2540 AGTGAAGACCTCTTCAATCTAGCGGTTCTCTGAGGGAATAAATTTAGAA-----ATTC 2593
Qy 2624 TGCAAGATGCAACGTACATCTAACTCTTGGTTATATCTGTGGATCTTGTTCGTAGTAAC 2683
Db 2594 TCCGATAAGCTACGTATGATCTCTCCATAGCTTACGTTCCCGATGTGATTCGTATGAT 2653
Qy 2684 CCCGCTGTACGACAACTCGGAATTTAGCGGTGATTTCTTGGAAACCTTCGTTACGAAT 2743
Db 2654 CCAGGCTGCACGACAACTCTTATGGTTTCTGGGGATTTCTGGTGCACATGTGTACAGC 2713
Qy 2744 TTGCGACAGCAAGCTTTAGTCTTCTGTCGAGGGAACCATTTTGTCTTAACTCAAAATTTT 2803
Db 2714 TTGCTAGACAGGCTCTTCTTGTACGTGCTGGAAATCATCATGCTTGTCTTCAACTTT 2773

Qy 2804 GAAGCTTTAGCCAAATTTCTTTTGAATTCGTTGGTCAATCTCGCAATTCATATGATGAC 2863
Db 2774 GAAGTTTTCAGTCACTTTGAAGTCGAGTTGGAGGTTCTTCTCGTAGCTATGCTATCGAT 2833
Qy 2864 TTAGAGCAAAATACCAATTTCTTAATGC 2890
Db 2834 CTTGAGGAAGATTCGGATTTTAATCC 2860

RESULT 12

ABL91192 standard; DNA; 534 BP.

AC ABL91192;

XX 29-AUG-2003 (revised)

DT 29-JUL-2002 (first entry)

XX Chlamydia pneumoniae cp0014 ORF DNA, SEQ ID NO:18.

XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW human respiratory disease; cardiovascular disease; atherosclerosis;
KW coronary artery disease; carotid artery stenosis; myocardial infarction;
KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW strain CWL029; open reading frame; ORF; gene; ds.

XX Chlamydia pneumoniae.

Key Location/Qualifiers

FT 1..534

FT /*tag= a

FT /product= "cp0014"

XX WO200202606-A2.

XX 10-JAN-2002.

XX 03-JUL-2001; 2001WO-IB001445.

XX 03-JUL-2000; 2000GB-00016363.

XX 11-JUL-2000; 2000GB-00017047.

XX 21-JUL-2000; 2000GB-00017983.

XX 07-AUG-2000; 2000GB-00019368.

XX 18-AUG-2000; 2000GB-00020440.

XX 14-SEP-2000; 2000GB-00022583.

XX 10-NOV-2000; 2000GB-00027549.

XX 22-DEC-2000; 2000GB-00031706.

XX (CHIR-) CHIRON SPA.

XX Ratti G, Grandi G;

XX WPI: 2002-154726/20.

XX N-PSDB; ABB90534.

XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes.

XX Claim 5; Page 49; 364pp; English.

XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC them. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as
CC atherosclerosis, coronary artery disease, carotid artery stenosis,
CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC claudication and stroke. The proteins and nucleic acids of the invention
CC may be used in vaccines and pharmaceutical compositions for the
CC prevention or treatment of chlamydial infections, particularly Chlamydia

CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 534 BP; 147 A; 105 C; 117 G; 165 T; 0 U; 0 Other;

Query Match 17.4%; Score 523; DB 6; Length 534;
 Best Local Similarity 39.8%; Pred. No. 1.4e-134;
 Matches 534; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 101 ATGAAGTCTTCTTTCCCAAGTTGTATTTCTACATTTGCTATTTTCCCTTTGCTATG 160
 Db 1 ATGAAGTCTTCTTTCCCAAGTTGTATTTCTACATTTGCTATTTTCCCTTTGCTATG 60
 QY 161 ATTGCTACCGAGACAGTTTGGATTCAAGTGGGATTCGATGGGAATAAAATGGTAA 220
 Db 61 ATTGCTACCGAGACAGTTTGGATTCAAGTGGGATTCGATGGGAATAAAATGGTAA 120
 QY 221 TTTTTCAGTTCGTGAGTACGAGGAGTCTGGAATCTTAAAGGGAATGTC 280
 Db 121 TTTTTCAGTTCGTGAGTACGAGGAGTCTGGAATCTTAAAGGGAATGTC 180
 QY 281 ACTCTAGAAATATTCCTGGAAACAGGCACAGCAATCAAAAAAGCTGTTTAAACAACACT 340
 Db 181 ACTCTAGAAATATTCCTGGAAACAGGCACAGCAATCAAAAAAGCTGTTTAAACAACACT 240
 QY 341 AAGGGGATTTGACTTTACAGTAACGGGAATCTCTATTGTTCCAAACGGTGGATGCA 400
 Db 241 AAGGGGATTTGACTTTACAGTAACGGGAATCTCTATTGTTCCAAACGGTGGATGCA 300
 QY 401 GGGAGTGTACGGGCTGCTGTTTACAGCAGCGTGTAGATAAATCTACAGTTTATA 460
 Db 301 GGGAGTGTACGGGCTGCTGTTTACAGCAGCGTGTAGATAAATCTACAGTTTATA 360
 QY 461 GGGTTTTCTTCGCTATCTTTTATTGCGTCTCTCGAAGTTTCGATACTACCGCAAGGA 520
 Db 361 GGGTTTTCTTCGCTATCTTTTATTGCGTCTCTCGAAGTTTCGATACTACCGCAAGGA 420
 QY 521 GCGTTAGTCTCTACGGTAGCTTGAATTCGACAAAATCTCAGTTTGTCTTTCAGC 580
 Db 421 GCGTTAGTCTCTACGGTAGCTTGAATTCGACAAAATCTCAGTTTGTCTTTCAGC 479
 QY 581 AAAAATCTTTCAACGATATGCGGTGCTATCACCGCAAAATCTTTCATTTAA 635
 Db 480 AAAAATCTTTCAACGATATGCGGTGCTATCACCGCAAAATCTTTCATTTAA 534

RESULT 13

AXX06821

ID AAX06821 standard; DNA; 2757 BP.

XX AC AAX06821;

XX DT 17-OCT-2003 (revised)

DT 26-APR-1999 (first entry)

XX DE Chlamydia pneumoniae surface exposed protein Omp9 DNA.

XX KW Omp9; outer membrane protein 9; surface exposed protein; antigen;

XX LW infection; diagnosis; vaccine; atherosclerosis; asthma; ss.

XX OS Chlamydia pneumoniae.

XX PN WO9858953-A2.

XX PD 30-DEC-1998.

XX PF 19-JUN-1998; 98WO-DK000266.

XX PP 23-JUN-1997; 97DK-00000744.

XX PA

XX PA

XX XX

XX PI

XX XX

XX DR

XX DR

XX XX

XX PT

XX PT

XX PT

XX XX

XX PS

XX XX

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX SQ

Sequence 2757 BP; 770 A; 564 C; 642 G; 781 T; 0 U; 0 Other;

Query Match 17.4%; Score 522.2; DB 2; Length 2757;

Best Local Similarity 53.4%; Pred. No. 5.3e-134;

Matches 1424; Conservative 0; Mismatches 1153; Indels 90; Gaps 12;

QY 242 GAAGATGCTGGAACTACCTATTTAAGGGAATGCTCACTAGAAATATTCCTGGA 301

Db 160 GATGCTAGTGGACGACCTATATTTCTGATGGGATGCTCGATA--AGCCAAGCAGGG 216

QY 302 ACAGGCACAGCAATCAAAAAAGCTGTTTAAACAACATAAGGGCGATTTGACTTTTACA 361

Db 217 AAACAAACGAGCTTAACCAAGTTGTTTCTAACACTGCAGGAATCTTACCTTTCTTA 276

QY 362 GGTACCGGAATCTCTATTGTTTCCAAACGGTGGATGCGAGGACTGTAGCGGGCTGCT 421

Db 277 GGGACCGGATTTCTCTCATTTTGACAATATATTTCGTCTACTGTGCGAGTGTGTT 336

QY 422 GTTACACAGCAGCTGTAGATAAATCTACACGTTTATAGGGTTTCTTCGCTATCTTT 481

Db 337 GTTAGCAATACAGCCTTCTGGGATTCAGAAATCTCAGGATTTTCAACTCTTCGAGT 396

QY 482 ATTGGCTCTCTCGAAGTTTCGATACTACCGCAAGGAGCGGTAGCTGCTACGGGT 541

Db 397 CTTCGAGCTCTCT-----AGGACCACAGGTAAAGAGCCATTA--AAATTACCGAT 444

QY 542 ACCTTGAGTTTGACAAAAATCTAGTTTGTCTTCAGCAAAAATCTTTTCAACGGATAAT 601

Db 445 GGTCTGGTGTGAGAGTATAGGAATCTTGACCAAAATGAAATGCCCTCTAGTGAAT 504

QY 602 GCGGTGTCTATCACCGCAAAATCTTTCATTTAAACAGGACTACAAATGTCAGCTCTGTT 561

Db 505 GGGGAGCCATCAATACGAGACTTTGCTTTTGACTGGGAGTACGGGTTTGTAGCGTTTC 564

QY 662 TCTGAAATACCTCTCTCAAGAAAGCGGAGCAATTCAGACTTCGATGCCCTTACCATTT 721

Db 565 CTTGGCAATAGCTCTCGCAACAGGGGAGGAGTCTATGCTTCTGGTGAATCTGTGATT 624

(BIRK/) BIRKELUND S.
 (CHRI/) CHRISTIANSEN G.

Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;

WPI: 1999-105610/09.

P-PSDB; AAW06822.

Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding these proteins.

Claim 6; Page 55-56; 115pp; English.

This DNA sequence codes for the novel 96.7 kDa surface exposed protein Omp9 (see AAW89422) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX04816-27) encoding Omp4-Omp15 proteins (see AAW89417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89,6-100,3 kDa and about 56,1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae. (Updated on 17-OCT-2003 to standardise OS field)

QY 722 ACTGGAACCAAGGGAAGTCTCTTTTCTGACAAATCTCTTTCGGATTCTGGAGCTGCA 781
DB |||||
QY 625 TCTGAGAATCAGGGAATCTTGAGCTTCGGAACCAACAGTGCACAAATCAGAGGCGG 684
DB |||||
QY 782 ATTTTACAGAGCCTCGGTGACTATTTCTTAATATGCTAAAGTTTCCTTTATTTGACAAAT 841
DB |||||
QY 685 ATCTCTGCTGAGGGAACCTTGATGATCTCCAAATACCAAAATATCTTTTCGATGGCTGC 744
DB |||||
QY 842 AAGGTCA CAGAGCGAGCTCTCAACAGCGGGGATATGTCAGGAGGTGCTATCTGTGCT 901
DB |||||
QY 745 AAAGCAACTACAAATGCGGAGCTATTTGATTTGTAACAAAGCAGGGG----- 790
DB |||||
QY 902 TATAAACTAGTACAGATACTAAGGTCAACCTCACTCGGAATTCAGATGTACTCTTCAGC 961
DB |||||
QY 791 -----CGAACCCAGACCTATCTTGACTCTTTTCAGGAATGAGGCTGCAATTTCTG 843
DB |||||
QY 962 AACATACTACACACAGCGGAGGAGCTATCTATGTGAAAGCTCGAATCGCTGCC 1021
DB |||||
QY 844 AATAACACAGAGGAATAGTGGAGGTGCGAATTTATACCAAAATTTGGTGTATCTCTCA 903
DB |||||
QY 1022 GGAGACTTACCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCTTAAGGTGA 1081
DB |||||
QY 904 GGACGAGGAGGAGTGTATTTTCTAACCAAAAGCTGGAATGCTACTCTTAAGGAGGG 963
DB |||||
QY 1082 GCATAGCTATCGAAGATAGTGGGAAATTTGAGTTTATCCGCCGATAGTGGTGACATTTGTC 1141
DB |||||
QY 964 GCAATTCGATCTAGATTTCTGGAGAGATAGCAATTTCTGCAGATCTCGGCAATATCAT 1023
DB |||||
QY 1142 TTTTTAGGGAATPACAGTCTACTCTAC-----TACTCTGGGACCAATAGAGTAGTATC 1195
DB |||||
QY 1024 TTCGAGGGCAATACTACGAGCACTACAGGAAGTCTCTCGAGTGTGACCAAAATGCTATA 1083
DB |||||
QY 1196 GACTTAGGAACGAGTGCAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGGCCATCTAC 1255
DB |||||
QY 1084 GATCTGCAATGCAAAATTTTAAATCTCCGAGCGACTCGGGGAAATAAAGTTATT 1143
DB |||||
QY 1256 TTCTATGATCCCATACTACAGGATCATCCACAAGTTACAGATGTCTTTAAAGTTAAT 1315
DB |||||
QY 1144 TTCTATGATCTTATCAGA-----GCTCAGGAGCTACTGATAGTCTCTTTGAT 1194
DB |||||
QY 1316 GAGACTCCGGCAGATTTCTGCACCTACAAATATACAGGGAACATCATCTTTCACAGAGAAAG 1375
DB |||||
QY 1195 AAAGCTGACGAGGACTCTGGAATACCTATGAAGCTACATCGTTTCTCTGAGAGAAA 1254
DB |||||
QY 1376 TTATCAGACACAGAGCCCGAGATTTCTAAATCTTACTTCGAAGTACTACAGCCTGTA 1435
DB |||||
QY 1255 CTCTCAGAGAGGAACCTTAAGAAACCTGAAATCTGAAAGTCTACATTTACAGAGGCTGTA 1314
DB |||||
QY 1436 ACTCTTTTCAGGAGGTACTCTATCTTTAAACATGGAAGTGAATCTGCAGACTCAGGCAATC 1495
DB |||||
QY 1315 GAGCTTCTGCAGTGCCTTAGTATTTGAAGATGGAGTGAATCTAGTTGCAATACTATA 1374
DB |||||
QY 1496 ACTCAACAGCGAGATTTCTCGTCTCGAAATGGAGGTAGGAATCTACTCTAGA-----ACCTGCT 1552
DB |||||
QY 1375 ACGCAGCTCGAGGATCGAAAGTCGTTATGATGAGGAGGACTACTTTTTCAGGCAAGCGCT 1434
DB |||||
QY 1553 GATACTAGCACCATAACAAATTTGGTCAATTAACATCAGTTCTATAGACGTGCAAGAGAG 1612
DB |||||
QY 1435 GAGGGGTCACTCTCAATGGCCCTAGGCCATTAATAGATTCCTTAGATGGGCAATATA 1494
DB |||||
QY 1613 GCAAAATAGAAACCAAGCTAGCTCAAAATATCTGACTTTTATCTGGAACCACTACTTTA 1672
DB |||||
QY 1495 GCTATCATTAAGCGGACGCGAGCAAGTAAGGATTTGCCCTTATCAGGGCCTATCATGCTT 1554
DB |||||
QY 1673 TTGGACCGAGCGGCGAGTTTATGAAATCATAGTTTAAAGAAATCTCTAGTCTCTAGAC 1732
DB |||||
QY 1555 GTAGATGCTCAGGGGAATATTATGAGCATCAATAATCTCAGTCAACAGCAGGCTTTCTCT 1614
DB |||||
QY 1733 ATCTTAGAGCTCAAGCTCTCGAATGTAAACAGACCGCAGTGAATCCAGATCTCTATA 1792
DB |||||
QY 1615 TTAAATAGACTTTCTGCACAAAGAACGATGACTACTACAGATATCCCGGATACCCCAATT 1674
DB |||||

QY 1793 ATGGGTGAGAAATTCATTTACGGGTATCAGGGAACTTGGGGCCCAATTTGTTTGGGGACA 1852
DB |||||
QY 1675 CTAATACTACGAATCACTATGGGTATCAGGAACT---GGAATAAATTTGTTGGTTCGAC 1731
DB |||||
QY 1853 GGGGCTTCT-----ACGACTGCAACCTTCACTGACTTAAACTGGGTATATTTCT 1903
DB |||||
QY 1732 GATGCACTGCAAAACAAAAAATGCTACCTTTAATCTTGACTTAAACAGGATACAGCGG 1791
DB |||||
QY 1904 AATCCGAGCGTATCGGCTCTTTTAGTCCCTAATAGCTTTATGGAAATGCAATTTATAGATTT 1963
DB |||||
QY 1792 AATCAGAACTCAGGACCTTTTGGTCTTAATAGCTTGGGGTCTTTTGTGCGATGTC 1851
DB |||||
QY 1964 AGCTCTCTCCATTTATTTATGGAGACTGCAACAGAGGGTTGCAGGAGACCGTCTTTT 2023
DB |||||
QY 1852 CGCTCAATTCAGAGCCTCATGGACGAGCAAGTTCGTTTATCTTCGTCACAAATTTG 1911
DB |||||
QY 2024 TGCTGTGCTGATTTATCTAACTTCTCCATAAGGATAGTACAAAACACAGCGGGTTT 2083
DB |||||
QY 1912 TGGGTATCAGGAATCGCGACTTTTGGTATGATGAGATCAGAAAGGAACCAAGTAGTTAT 1971
DB |||||
QY 2084 CGCCATTTGAGTGGCGTTATGTCTATAGGAGGAAAACCTACATPACTTGTTCAGATAAGATT 2143
DB |||||
QY 1972 CGTCATTTAGCGGGTTATGCAATTAGGAGGAGTCTTTCACGGCTTCGAAAAATTC 2031
DB |||||
QY 2144 CTTAGTGTGCAATTTTGTTCAGCTCTTTTGAAGAGATAGAGACTCTTTGTAGCTAAGAT 2203
DB |||||
QY 2032 TTTAATTTTGGCTTTTGTTCAGCTTTTGGCTACGACAGGACCCTCTTTGTGGCTAAGAAC 2091
DB |||||
QY 2204 CAAGGTACAGTCTACGGAGGAACTCTCTATTACAGACCAACGAAACCTATATCTCTTT 2263
DB |||||
QY 2092 CATACCCATGATNATGAGGGGCAATGAGTTACCGACACTCGGAGAGTCTAAGACCTC 2151
DB |||||
QY 2264 CTTTGCAAACTACGGCCTTTGTTGTTTGTCTTAATGTTCTCTACAGAGATTCCTGTTCTCTTT 2323
DB |||||
QY 2152 GCTAAGA-----TTTTGTGAGGAATTTCTGACTCCCTACTCTTTGTGCTTC 2196
DB |||||
QY 2324 TCAGAAACCTTAGCTACACCCATAGGATACGATCTGAAACCAAGTATACACATAT 2383
DB |||||
QY 2197 AATGTCGGTTTGTCTTATGGCCATACCGACAATAACATGACCACAAAGTACACTGGCTAT 2256
DB |||||
QY 2384 CTTACTGTTTAAAGGAAGCTGGGGGATGATAGTTTCGCTTTAGAAATTCGGTGAAGAGCT 2443
DB |||||
QY 2257 TCTCTGTTTAAAGGAAGCTGGGGAAATGATGCTTCGGTATAGAAATGCGAGGAGCTATC 2316
DB |||||
QY 2444 CCGA---TTTGTCTTAGATGAAAGTGTCTTATTTGAGCAGTACATGCCCTTCATGAAATTG 2500
DB |||||
QY 2317 CCGGTAGTTGCTTCAGGAGCTCGGTCTTGGTGGATACCCACACGCAATTTCTAAACCTA 2376
DB |||||
QY 2501 CAGTTTGTCTATGCACATCAGGAAGTTTAAAGACAGGGAACAGAGCTCGTGAATTT 2560
DB |||||
QY 2377 GAGATGATCTATGCACATCAGAAATGACTTTAAGGAAACCGGACAGAGCGGCTCTTTC 2436
DB |||||
QY 2561 GGAAGTACGCGCTTGTGATCTTGGCTTACCTATCGGGATCCGATTTGATAGGAATCA 2620
DB |||||
QY 2437 CAAAGTGAAGACTCTTCAATCTAGCGGTTCCTGTAGGGATAAAATTTGAGAA-----A 2490
DB |||||
QY 2621 GACTGCCAAGATGCAACGTFACAAATCTTCTTGTGTTTACTGTGATCTTGTTCGTAGT 2680
DB |||||
QY 2491 TTTCTCGATAAGTCTACGTATGATCTCTCCATAGCTTACGTTCCCGATGTGATTCGTAAT 2550
DB |||||
QY 2681 AACCCGACTGTACGACACACTCGCAATTAGCGGTGATTTCTTGGAAAACCTTCGGTACG 2740
DB |||||
QY 2551 GATCCAGGTGACGACAACTCTTATGGTTTCGCGGATTTCTTGGTCGACATGTTGATCA 2610
DB |||||
QY 2741 AATTTGGCAAGCAAGCTTTAGTCTTTCGTCAGGGAACCAATTTTGTCTTAACTCAAAAT 2800
DB |||||
QY 2611 AGCTTGTCTAGACAACTCTTCTTGTACGTGCTGGAATCATCATGCTTTGCTTCAAAAC 2670
DB |||||
QY 2801 TTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGGTGGGTGCTCTCGCAATTTACAAATGTA 2860
DB |||||
QY 2671 TTTGAAGTTTTCAGTCAGTTTGAAGTCGAGTTCGAGGTTCTTCTCGTAGCTATGCTATC 2730
DB |||||
QY 2861 GACTTAGGACAAAATACCAATTTCTAA 2887
DB |||||

Db 2731 GATCTTGGAGGAATTCGGAATTTAA 2757

RESULT 14

AAx91990_05

Continuation (6 of 13) of AAx91990 from base 500001 (Nucleotide sequence of the complete
 WP Sequence split into 13 fragments LOCUS AAx91990 Accession AAx91990

Fragment Name	Begin	End
WP AAx91990_00	1	110000
WP AAx91990_01	100001	210000
WP AAx91990_02	200001	310000
WP AAx91990_03	300001	410000
WP AAx91990_04	400001	510000
WP AAx91990_05	500001	610000
WP AAx91990_06	600001	710000
WP AAx91990_07	700001	810000
WP AAx91990_08	800001	910000
WP AAx91990_09	900001	1010000
WP AAx91990_10	1000001	1110000
WP AAx91990_11	1100001	1210000
WP AAx91990_12	1200001	1230025

Query Match 17.3%; Score 518.4; DB 2; Length 110000;
 Best Local Similarity 52.8%; Pred. No. 3.6e-132;
 Matches 1409; Conservative 0; Mismatches 1201; Indels 60; Gaps 11;

QY 250	TGGAACCTACCTACTATTTAAAGGGAATGTCATCTAGAAAATATTCCTGGAAACAGGCAC	309
Db	7879 TGGACGAACATGATCTTATCAGGAATGCTATATAACGA---TGCTGGGAAGGCAC	7935
QY 310	AGCAATCACAAAAGCTGTTTTAACACACTAAGGCGATTTTCACCTTTCACAGSTAACGG	369
Db	7936 AGCATTAAACAGGCTGCTCTTTACAGAAACTACGGGTGATCTGACATTTACTGGAAGGG	7995
QY 370	GAACCTCTATTCTCCAAACGGTGGATCAGGACTAGCAGGGGCTGCTGTTAAACAG	429
Db	7996 ATACTCATTTTCATCAACACGGTAGATCGGGTTCGAATGCAAGGAGCTGCGG---CAAG	8052
QY 430	CAGCGTGGTAGATAAATCTACCACTTTATAGGGTTTTCTTCGTATCTTTTATTCGGTC	489
Db	8053 CACAACCTGCTGATAAAGCCCTAACATTCACAGGATTTCTTAACCTTTCTTCATTGCAGC	8112
QY 490	TCTGTGAAGTTGATAACTACCGGGAAGAGCCGTTAGCTGCTCTACGGGTAGCTTAG	549
Db	8113 TCTGTGAACCTACAGTTGCTTCAGGAAAAAGTAGTCTTTAA---GTTCTGCAGGAGCCTTAA	8169
QY 550	TTTGACAAAAATGTCCAGTTTGTCTTCAGCAAAAACCTTTCAACGG-----ATAA	600
Db	8170 TCTTACCGATATGGAACGATTCCTTTAGCMAAACGCTCCCATGAAGCTAATAACAA	8229
QY 601	TGCGGTGCTATCACCGCAAAAACCTTTTCATTAAACAGGAGCTCAAAATGTCAGCTCTGT	660
Db	8230 TGCGGAGCGATCACCGCAAAAACCTTTTCATTCTGGAATACCTCTTCTATAACCTT	8289
QY 661	TTCTGAATACTCTCTCAAGAAAGCGGAGCCATTCAGACTTCGGATGCCTTACCAT	720
Db	8290 CACTAGTAATAGCGCAAAAAAATTTAGGTGGAGCGATCTATAGCTCTGCGGCTGCAAGTAT	8349
QY 721	TACTGGAACCAAGGGAAGTCTCTTTTCTGACATACTTCTTCGGATTCTTGGAGCTGC	780
Db	8350 TTCAGGAACACCGGCCAGTTAGTCTTTATGATATAAAGGAGAACTGGGGGTGGGGC	8409
QY 781	AATTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCTTTTATTGACAA	840
Db	8410 TCTGGGCTTTGAAGCCAGCTCCTCGATTACTCAAAATAGCTCCCTTTCTCTCTGGAA	8469
QY 841	TAAAGTTCAGAGGAGCGACTCCTCAACACGGGGGATATGTCAGGAGGTCTATCTGTGC	900
Db	8470 CACTGCAACAGATGCTGCAAGCAAG-----GGCGGGGCCATTTATTG	8511
QY 901	TTATAAACTAGTACAGATACTAAGGTCACTCCTGGAATCAGATGTTACTCTCAG	960

Db 375 GCCACGGCTACCAATTTCTCCTCAAAAATATCGATCGGG-----AGCGAACTGTACCT 428
Qy 423 TTAACAGCAGCGTGTAGATAAACTACCAAGTTTATAGGGTTTTCTTCGCTAICTTTTA 482
Db 429 TTACCAATACAGCTGCAAAATAGCTTCTCTCTTTTCAGGATTTCTCTATTGTCACTAA 488
Qy 483 TTGGGTCTCTCTGGAAGTTTCGATAACTACCGGCAAGGAGCGGTAGCTGCTCTACGGGTA 542
Db 489 TACAAACCAACGAATGCT-----ACCACAGGAACAGGAGCCATCAAGTCCACAGAGCTT 542
Qy 543 GCTTTGAGTTTGACAAAATAGTGTGCTTCTTCAGCAAAAACCTTTTCAACGGATAATG 602
Db 543 GTTCTATTTCAGTCGAACTAT---AGTTGCTACTTTTGGCCAAAACCTTTTCTAATGACAATG 599
Qy 603 GCGGTGCTATCACGCAAAAACCTTTTCATTTAAACAGGAGCTACATGTCTCAGCTCTGTTTT 662
Db 600 GAGGCGCCTCAAGGCGAGCTCTATCAGTCTATCGCTAAACCCCAACCTAAC---GTTTG 656
Qy 663 CTGAAAATPACCTCTCAAGAAAGGCGGAGGCAATTCAGACTTCCGATGCCCTTACCATT 722
Db 657 CCAAAAACAAGCAACGCAAAAAGGGGTGCCCTTATTCCACGGGAGGATTAACAATTA 716
Qy 723 CTGGAACCAAGGGAAGTCTCTTTTCTGCAATATCTTCTTCGGAATCTCGAGCTGCAA 782
Db 717 ACAATACGTTAAACTCAGCATCATTTTCTGAAAATACCGCGCGCAACAATGGCGAGCCA 776
Qy 783 TTTTTCAGAAAGCCTCGGTGACTATTTCTAATAATGCTAAGTTTCTTTTATTCACRATA 842
Db 777 TTTTACAGGAAGCTAGCAGTTTATAGCAGCAACAAGCAATTAGCTTTTATAACAATA 836
Qy 843 AGGTCACAGGACGAGCTCTCAACAAGGGGGATATGTCAGGAGGTGCTATCTGTGCTT 902
Db 837 GTGTGACG-----CAACCTCAGCTACAGGGGGAGCCATTTACTGTAGTA 881
Qy 903 ATAAAATAGTACAGATCTAAGGTACCTCACTGGAATTCAGATTTACTCTPTCAGCA 962
Db 882 GTACATCAGCCCCCAACCCAGTCTTAATCTATCAGACAACCGGGAACCTGAACCTTTATAG 941
Qy 963 ACAATACATCGACAACGCGGAGGAGCTATCTATGTGAAAAGCTCGAACTGGCTCCG 1022
Db 942 GAATACAGCAATTTACTAGTGTGGGGGATTTATCTGCAATCTATGTTCTTTCTTCTG 1001
Qy 1023 GAGGACTTACCTTATCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCCTAAAGGTGGAG 1082
Db 1002 GAGGACCTACGCTTTTAAAAACAACCTGSCATATGATCTGACGCTCCCTTAGAGGAG 1061
Qy 1083 CCATAGTATCGAAGATAGTGGGAATAGTATTATCGCGGATAGTGGTGACATGTCT 1142
Db 1062 CAATTGGGATTTGCTGACTCTGGATCTTTGAGTCTTTGGGTCTTTGGTGAGACATCACTT 1121
Qy 1143 TTTTAGGGAATACAGT-----CACTTCTACTACTCTCGGAGCAAGATAGTAGTA 1193
Db 1122 TTGAAGAAACACAGTAGTCAAGGAGGCTTCTTCGAGTCAGACCCTACCAGAAATCTTA 1181
Qy 1194 TCGACTTTPAGG---ACGAGTGCAAGATGACAGCTTTTCGCTTCTGCTGGGTAGAGCCA 1250
Db 1182 TTAACATCGGAACACCAATGCTAAGATTTGACAGCTGGAGCTCTCAAGGCATACTA 1241
Qy 1251 TCTACTTCTATGATCCCAATTAACAGATCATCCACAAGTTTACAGATGTCTTAAAG 1310
Db 1242 TCTACTTCTATGATCCCTATAACAACCTAGCATCACTGCAAGTCTCTCAGATGCTCTAACT 1301
Qy 1311 TTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGAAACATCATCTTCACAGGAG 1370
Db 1302 TAAATGGTCTGACCTTGAGGGAATCCTGATATCAAGGAACCATCGTATTTTCTGGAG 1361
Qy 1371 AAAAGTTATCAGACAGAGCCGAGATTTCTAAAAATCTTACTTCGAAGCTACTACAGC 1430
Db 1362 AGAAGCTCTCGGAAGCAGAGCTGCAAGCTGATATCTCAATCTACAAATTCAGCAAC 1421
Qy 1431 CTGTACTCTTTCAGGAGGTACTCTATCTTTTAAACATGAGTACTCTGCAGACTCAGG 1490
Db 1422 CTCTAACTCTTGGGGAGGGCAACTCTCTCTTAAATCAGGAGTCACTCTAGTTGCTAAGT 1481

Qy 1491 CATTCACCTACACGACAGATTCTCGTCTCGAAAATGGAGCTAGGAACACTACTCTAGAACCTG 1550
Db 1482 CTTTTTCGCAATCTCCGGGCTCTACCTCTCATGGATGCGAGGACCAATTTAGAAACCG 1541
Qy 1551 CTGATACTAGCACCATAAAACAATTTGGTCAATTAACATCAGTTCTATAGACGGTGCAGAGA 1610
Db 1542 CTGATGGGATCACTATCAATTAATCTTGTCTCAATGTAGATTCTTTAAAGAGACCAAGA 1601
Qy 1611 AGGCAAAAATAGAAACCAAGCTACGTCAAAAATCTGACTTTTATCTGGAAACCACTCACTT 1670
Db 1602 AGGCAACGCTAAAAGCAACAACGAAGTCAGACAGTCTTATCTGATCGCTCTCTC 1661
Qy 1671 TATTGGACCGACGCGGACGTTTTTATGAAAATCATAGTTTAAAGAAATCCTCAGTCTTACG 1730
Db 1662 TTGTAGATCTCTTCTGGAATATGCTACGAAGATGTCTCTTGAATAAACCTCAAGTCTTTT 1721
Qy 1731 ACATCTTAGAGCTCAAAAGCTT-----CTGGAACGTGTAACAGCACCGCAGTGCCTCAG 1784
Db 1722 CTTGTCTCACTTTACTGTCTGACGACCCCGGAATATTTCACTCACAGACTTAGCTGCTG 1781
Qy 1785 ATCCTATAATGGGTGAGAAAATTCATTTACGGCTATCAGGGAACCTTGGGGCCCAATTTGTT 1844
Db 1782 ATCCCTTAGAAAAAATCCCTATCATTTGGGGATACCAAGGGAATTTGGCATTATCTTTGGC 1841
Qy 1845 GGGGGACAGGGGC-----TTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATA 1898
Db 1842 AAGAGGATACCTGGACTTAAATCCAAAGCAGCGACTCTTACTCGACAAAAACAGGATACA 1901
Qy 1899 TTCTTAATCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTATGAAATCATTATTAG 1958
Db 1902 ATCCGATCTGAGCGTCTGGTGGACCTTAGTTGTCTTAACGCTATGGGATCTTTTGTG 1961
Qy 1959 ATATTAGCTCTCCCAATTATCTTATGGAGACTGCAAAACGAAGGTTTCAGGAGACCGCTG 2018
Db 1962 ATGTGCGCTCCATACAACAGCTTGTGCCACTTAAAGTACGCCAATCTCAAGAAACTCGC 2021
Qy 2019 CTTTTTGGTGTGCTGATTATCTAACTTCTTCATAGGATAGTACAAAACACAGACGCG 2078
Db 2022 GCATCTGCTGTAAGGGATCTCGAACTTCTTCCATAAAGATAGCACGCAAGATAAATAAG 2081
Qy 2079 GGTTCGCCCAATTTGAGTGGGCTTATGTCATAGGAGAAACCTACATCTTGTTCAGATA 2138
Db 2082 GTTTTCGCCACATAAGTGAGGTTATGTTGTAGAGGCGCTACAACTTAGCTTCTGATA 2141
Qy 2139 AGATTTTAGTGTGCTATTTGTGAGCTCTTTTGGAGAGATAGAGACTACTTTTAGCTA 2198
Db 2142 ATCTTATCACTGACGCTTCTGCAATTTATTCGGGAAAGATAGAGATCACTTTTATAATA 2201
Qy 2199 AGAATCAGGTACAGTCTAGGAGGAACTCTCTATTAACGACACAACGAACCTATATCT 2258
Db 2202 AAAATAGAGCTTCTGCTATGCACTTCTCTCCATCTCCAGCATCTAGCAGCTTGTCTT 2261
Qy 2259 CTTCTCTGCAAACTAGGCGCTTGTGCTGTTCTTATGTTCTCTACAGAGATTCCTGCTC 2318
Db 2262 CTCGAGCTTGTAC-----GCTACCTCTCTGATCTGAAAGTGAGAGCGCTGTCC 2312
Qy 2319 TCTTTTCAGAAACCTTAGCTACACCCATACGGATAACGATCTGAAACCAAGTATACAA 2378
Db 2313 TCTTTGATGCTCAGATCAGCTATCTATATAGTAAAAATACTATGAAACCTTATACACC 2372
Qy 2379 CATATCTACTGTAAAGAGCTGGGGNAATGATAGTTTCGCTTTAGAAATTCG---GTG 2435
Db 2373 AAGCAAAAAGGAGAGAGCTCGTGTATATAATACGCTTTCGCTCTGGAACCTTGCAGCT 2432
Qy 2436 GAAGAGCTCGATTTGCTTAGATGAAAGTCTCTATTTTGAAGAGTACATGCCCTTCATGA 2495
Db 2433 CCCTACCAACACTGCTTTTAAAGCATGAGGCTCTCTTCACGCGTATTTTCTTTTCATCA 2492
Qy 2496 AATTGCAAGTTGTATGCAATCAGGAAGGTTTTTAAAGAAC---AGGGAAACAGAAAGCTC 2552
Db 2493 AAGTAGAAGCTTCGTACATACACCAAGATAGCTTCAAGAGACGTAATACTACTCTTGGTAC 2552

QY	2553	GTGAATTTGGAGTAGCCGTCTTTGGAATCTTGGCCCTTACCTATCGGGATCCGATTTGATA	2612
Db	2553		
QY	2613	AGGAATCAGACTGCCAAGATGCAACGTACAACTAACTTGGTTATATACTGTGGATCTTG	2672
Db	2613		
QY	2673	TTGCTAGTAAACCCGACTGTACGCAACAACACTCGGAATTAGCGGTGATCTTTGAAAAACCT	2732
Db	2673		
QY	2733	TCGGTACGAATTTGGCAAGCAAGCTTTAGTCTTCGTCAGGGAACCAATTTTGTCTTTA	2792
Db	2733		
QY	2793	ACTCAAAATTTGAAGCTTTAGCCAAATTTCTTTGAATTTGGTGGTGCATCTCGCAATT	2852
Db	2793		
QY	2853	ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAA	2887
Db	2853		

Search completed: August 16, 2004, 15:10:01
Job time : 793 secs


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Best Local Similarity 34.5%; Pred. No. 0.11;
Matches 129; Conservative 66; Mismatches 178; Indels 1; Gaps 1;

QY 29 TTCTTGACTGCTCTCTCTCTATTCGTGTATCTCTTAAATAATTAATAATCAAAAGT 88
   ||| ||| ||| : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 909 TTTTCTTTTTTTTAAATWAWTTTTTATATTTTAAATAATTTAAATAAAWTTTTTTT 850
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 89 ATATATTTTACAATGAAGTCTCTTCTCCCAAG-TTTGTATTTTCTACATTGCTATTTT 147
   ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| ||| ||| |||
Db 849 TTWTWTWTWTWAWTAADTTTATWKHYWHATGETKYYTITTTTBTTTTATAGKGGTTT 790
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 148 CCCTTTTGCTATGATGCTACCGAGACAGTTTGGATTCAAGTCGGAGTTTCGATGGAA 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 789 YCMRKADNNSNNHHMMHHMMHMASSSVCAAAKAGAYNCGWGMRKRAMWNVGAA 730
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 208 TAAAAATCGTAAATTTTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAAGTACCTACCTATT 267
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 729 AAAARMAAAAWAAVVAANDKNCSGNAGGGSGBBSFGAATMCGGNCACAKTTBTATT 670
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 268 TAAGGGAATGCTCACTAGAAATATTTCTTGGAAAGGCAGCAGCAATCAGAAAAAGCTG 327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 669 MGGAWACAMMAAAAAAAMAAAAAAGCAAGWATAAAGTCCTTWHAAAAATCAAAAAGGAA 610
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 328 TTTTAAACAACAATAAGCGCGATTGACTTTTCAGAGGTAAACGGGAATCTCTATTGTGCTCA 387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 609 ATMWABNBKBTBKBBAAATATTGTCATTGAATCCATTTWTGGAAAAAGKAGGGGTCTTA 550
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 388 AACGGTGGATGCAG 401
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 549 AGAGTKGGGGGAAG 536
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RESULT 3
 AU076383/c
 LOCUS
 DEFINITION AU076383 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
 discoideum cDNA clone SSA686, mRNA sequence.
 ACCSSION
 VERSION AU076383
 KEYWORDS AU076383.1 GI:5607281
 SOURCE EST.
 ORGANISM Dictyostelium discoideum
 Dictyostelium discoideum
 Rukaryota; Mycetozoa; Dictyosteliida; Dictyosteliida.
 1 (bases 1 to 334)
 Urushihara,H.
 DEVELOPMENTAL cDNA in Dictyostelium discoideum (1999)
 UNPUBLISHED (1999)
 CONTACT: Hideko Urushihara
 Institute of Biological Sciences
 University of Tsukuba
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
 TEL: 81-298-53-4664
 FAX: 81-298-53-6614
 EMAIL: hideko@biol.tsukuba.ac.jp
 PROJECT = Dictyostelium discoideum cDNA project in Japan.
 LOCATION/Qualifiers
 1..334
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 FEATURES
 source

[illegible]

```

QY      89 ATATATTTTACAAATGAGTCTCTTCCCAAGTTTGTATTTTCTACATTTGCTATTTTC 148
Db      265 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 206

QY      149 CTTTCTGTATGATTCGTACCGAGACAGTTTTCGATTCAGTCCGAGTTTTCGATGGGAAT 208
Db      205 CTATTTTTCAGATATTTCTGTACACCTTTATYAGATTCGAAATGTTCTTTCAAAGATCT 146

QY      209 AAAAATGGTAATTTTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAACACTACCTACCTATTT 268
Db      145 AAATGTGGGAACCTTACCATTTGTATAGAGATCAGCAGCAAAATGTTAAACATTAACCAATG 86

QY      269 AAGGAAATGCTACTAGAAAATATTCCTGGACAGGACAGCAATCACA 319
Db      85 TATTCAAGCAACATAAACATATAATCAGCCAAAGTGTAAAGATTTACCA 35

RESULT 4
AU263143/c
LOCUS      AU263143 VS Dictyostelium discoideum cDNA clone VSE486 3', mRNA
DEFINITION
ACCESSION AU263143
VERSION   AU263143.1 GI:20519690
KEYWORDS  EST.
SOURCE    Dictyostelium discoideum
ORGANISM  Dictyostelium discoideum
REFERENCE 1 (bases 1 to 585)
AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriiki,E., Ochiai,H., Maeda,M.,
          Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE     Population analysis of cDNAs from unicellular and multicellular
          stages of Dictyostelium discoideum
JOURNAL   Unpublished (2002)
COMMENT   Contact: Hideko Urushihara
          Institute of Biological Sciences
          University of Tsukuba
          1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
          Tel: 81-298-53-4664
          Fax: 81-298-53-6614
          Email: hideko@biol.tsukuba.ac.jp.
FEATURES
source
1..585
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSE486"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

ORIGIN
Query Match      1.6%; Score 46.8; DB 9; Length 585;
Best Local Similarity 47.9%; Pred. No. 0.96;
Matches 135; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY      38 TTGTTTCTCCATGGTGTATCTCTTAAATATTAATCAAAATCAAAATCAAAATATATTTT 97
Db      584 TTGTTGTTGTTGTTGTTTACCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 525

QY      98 ACAATGAAGTCTTCTTCCCAAGTTTGTATTTTCTACATTCGATTTTCCCTTGTCT 157
Db      524 TTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 465

QY      158 ATGATTGTCACGACAGTCTTTCGATTCAGTGGAGTTTTCGATGGGAATCAAAATGCT 217
Db      464 AGATATTCGTACACCTTTATTAGATTCGAAATGTTCTTTCAAGAAATCTAAATGTGGG 405

QY      218 AATTTTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAACCTACCTATTTTAAAGGGAAT 277
Db      404 AACTTACCATTCGTATAGAGATCAGCAGCAAAATGTTAAACATTAACCAATGTTATTCATAA 345

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QY      278 GTCACTCTAGAAATATTTCTCTGGAACAGGCACAGCAATCACA 319
Db      344 GCAACATAACATATAAATCAGCCAAAGTGTAAAGATTTACCA 303

RESULT 5
BX336919
LOCUS      BX336919 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
DEFINITION
ACCESSION BX336919
VERSION   BX336919
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 1201)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 2019.r For
          more information about this cluster, see
          http://www.genoscope.cns.fr/
          cgi-bin/cluster.cgi?seq=CSODI033DF10QPI&cluster=2019.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Paraday Avenue Genoscope, sequence ID : CSODI033DF10QPI.
FEATURES
source
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI033YL20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      1.6%; Score 46.8; DB 13; Length 1201;
Best Local Similarity 39.4%; Pred. No. 1.1;
Matches 85; Conservative 36; Mismatches 95; Indels 0; Gaps 0;

QY      14 TAGAGTTGAGTGAATTTCTTGACTTCTCTCTATTCCTATGGTGTATCTTAAATATTA 73
Db      846 WATWBBTTTTTTATWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTT 905

QY      74 ATTCAAATCAAGTATATATTTTACAATGAAGTCTCTTCCCAAGTTTGTATTTCT 133
Db      906 ATWATWAWWAAATWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTT 965

QY      134 ACATTTGCTATTTTCCCTTTGCTGATGCTACCGAGACAGTTTGGATTCAGTGCG 193
Db      966 TTTTTTTATATTTTTHHTTTTTTTTTTTTATTTTAAATAMCCTCCCTTTTTTTTWTWTT 1025

QY      194 AGTTTCGATGGGAATATAAATGGAATTTTCAGTT 229
Db      1026 ATTAATAAATTTTTTTTWWHTTTTTTTTTTTTTTTTTT 1061

RESULT 6
BF265090/c
LOCUS      BF265090
DEFINITION HV_CEA0011D22f Hordeum vulgare seedling green leaf EST library

```

HVCNA0004 (Blumeria challenged) Hordeum vulgare subsp. vulgare
cDNA clone HV_CEA0011D22f, mRNA sequence.

ACCESSION
BF265090
VERSION
BF265090.3
KEYWORDS
GI:163334636
SOURCE
EST.

ORGANISM
Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.

REFERENCE
AUTHORS

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,
Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, J., Simmons, J.,
Choi, D.W., Fenton, R.D., Oates, R., and Main, D.

Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla13)
seedling leaf cDNA library

JOURNAL
COMMENT

Unpublished (2001)
On Nov 17, 2000 this sequence version replaced gi:13261889.
Contact: Wing RA

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

Email: rwing@clemson.edu

Total hg bases = 280

Seq primer: AATAACCTCTACTAAAGGG

High quality sequence stop: 831.

FEATURES

Location/Qualifiers

1..853

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="C16155 (Mla13)"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="HV_CEA0011D22f"

/tissue_type="seedling green leaf"

/lab_host="TUC121"

/clone_lib="Hordeum vulgare seedling green leaf EST

library HVCNA0004 (Blumeria challenged)"

/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;

C.I. 16155 (Mla13) plants were greenhouse grown in the R

Wise lab at Iowa State University, Ames, IA; 7 day old

green seedlings were challenged with isolate A27

were harvested 20 and 24 hr post-inoculation and snap

frozen; uninoculated leaves were harvested 20 hr

post-inoculation (Wei, Wise). In the TJ Close lab at the

University of California, Riverside, total RNA was

prepared from each sample pool, equal quantities of all

three RNA pools were combined, poly(A) RNA was purified

from the mixture, one cDNA library was made, and 1 million

pfu were in vivo excised to give phagescript SK(-) cDNA

phagemids (Choi, Close). Phagemids were plated and picked

at the Clemson University Genomics Institute (CUGI)

(Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA

preparations, DNA sequencing and sequence analysis were

performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,

Oates, Rambo, Main). The sequence has been trimmed to

remove vector sequence and contains a minimum of 100 bases

of phred value 20 or above. For more details on library

preparation and sequence analysis see

<http://www.genome.clemson.edu/projects/barley>. To order:

this clone see <http://www.genome.clemson.edu/orders> Also

see Close TJ, Wing R, Kleinhofs A, Wise R (2001)

Genetically and physically anchored EST resources for

barley genomics. Barley Genetics Newsletter 31:29-30.

(<http://wheat.pw.usda.gov/g9pages/bgm/31/cover.html>)"

ORIGIN

Query Match

Best Local Similarity 1.5%; Score 46.2; DB 10; Length 853;

Matches 57.8%; Conserv 57.8%; Indels 1.4;

Matches 78; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 29 TTCTTGTACTGTTTCTCCATATGTTGGTATCTCTTAAATATTAATTAATCAAGT 88
|||||
Db 808 TTTTATTTATTTGTTTAAATATNTAGTTTATATTATTTTAAAGTTGTTATTTTAT 749
|||||

QY 89 ATATATTTTACAATGAAGTCTTCTTCCCAAGTTTGTATTTTCTCAATTTGCTATTTTC 148
|||||

Db 748 ATNTTTTGTGCGAAATTTTATTTTATTAAGTTTATTTTATTTTATTTTATTTTTC 689
|||||

QY 149 CCTTGTCTATGATT 163
|||||

Db 688 CTTTATCTATATTT 674
|||||

RESULT 7

BZ643413/c

LOCUS

DEFINITION

BZ643413

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BZ643413 843 bp DNA linear GSS 29-JAN-2003
OGAOW57TM ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMA011J17,
genomic survey sequence.

BZ643413

BZ643413.1 GI:28104915

GSS.

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 843)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: OGAOW57TC

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..843

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMMBMA011J17"

/clone_lib="ZM 0.7_1.5_KB"

/note="Vector: pBGSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES

source

Query Match 1.5%; Score 45.4; DB 28; Length 843;
Best Local Similarity 49.8%; Pred. No. 2.3;
Matches 115; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 692 GCCATTGACACTTCGATGCCCTTACCACTTACTGGAACCAAGGGAAGTCTCTTTTCT 751
|||||

Db 552 GCTACTGCTGCTGCTGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTACTACT 493
|||||

QY 752 GACATACTTCTCGGATCTGGAGCTGCAATTTTACAGAAGCTCGTGACTATTTCT 811
|||||

Db 492 GCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACTACT 433
|||||

QY 812 AATAAGTGAAGTTTCCTTTTATTGACAAATAGGTACAGGAGCGAGTCTTCAACACG 871
|||||

Db 432 GCTGCTGCTACTACTACTGCTAACTACTACTACTACTGCTGCTGCTACTACTACT 373
|||||

QY 872 GGGGATATGTCAGGAGGTGCTATCTGCTTATATAAAGCTAGTACAGATCT 922
|||||

```
Db 372 GCTCTACTACTGCTACTGCTACTGCTTCTACTACTACTACTGCTACT 322

RESULT 8
BX376097/c
LOCUS
DEFINITION
BX376097 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC022YM12 5-PRIME, mRNA sequence.
ACCESSION
BX376097
VERSION
BX376097.1 GI:30434756
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2866.f
Contact: Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC022B060QF1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC022YM12"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
FEATURES
source
ORIGIN
Query Match 1.5%; Score 45.4; DB 13; Length 1201;
Best Local Similarity 8.8%; Pred. No. 2.4;
Matches 52; Conservative 236; Mismatches 299; Indels 1; Gaps 1;

QY 841 TAAGGTCACAGGACGAGCTCTCTCAACACGGGGGATATGTCAGAGGAGTCTCTGTC 900
Db 1032 TTTTCTTTTMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMKKMKKMKKMKKMKKMKK 973

QY 901 TTATAAACTAGTACAGATAGTACAGTCAACCTCACTGGAATCAGATGTTACTCTTCAG 960
Db 972 MKTKTMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMKKMKKMKKMKKMKKMKK 913

QY 961 CAACAAATACATCGAACACAGCGGAGGAGCTATCTATGTGAAAAAGCTCGAACTCGGCTC 1020
Db 912 GMMMMKMMMMMMGKGKGTGCGGGGMMVGMGGGMMVGMGGGMMVGMGGGMMVGMGGG 853

QY 1021 CGGAGGACTTACCCCTATTTCAGTAGAAATAGTGTCAATGAGAGGTACAGCTCTCTAAAGTGG 1080
Db 852 MMGNTDMKMTMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMM 793

QY 1081 AGCCATAGCTACAGATAGTGGGGAATTCAGTTTATCCCGCATAGTGGTGCATGTT 1140
Db 792 AAAAAAAGAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 733

QY 1141 CTTTATTAGGGAATACAGTCACTTCTACTACTCTCTGAGGAGAGAGAGAGAGAGAGAG 1200
Db 732 MMMMMMMKMMMMKMMMMKMMMMKMMMMKMMMMKMMMMKMMMMKMMMMKMMMMKMMMM 674

QY 1201 AGGAACGAGTGAAGATGACAGAGCTTTTCGCTGCTGCTGAGAGCCATCTACTCTTA 1260
Db 673 MMKXAGKMMNMMKMMKMMNMMNMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMM 614
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QY 1261 TGATCCCATAACTACAGGATCATCCACACAGTTTACAGATGTCTTAAAGCTTAATGAGAC 1320
Db 613 KMGKMMMGKAKANNMKKNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 554

QY 1321 TCCGGCAGATTCTGCACTACATATATACAGGGAACATCATCTTTCACAGGAGAAAGTTATC 1380
Db 553 MKNNNNNGKMGKNNNNNNAGKKKKMMNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 494

QY 1381 AGACACAGGCGCGCAGATCTTAAAAATCTTACTTTCGAAGCTACTACA 1428
Db 493 MNNMMMAAMMMGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 446

RESULT 9
AU263574/c
LOCUS
DEFINITION
AU263574 VS Dictyostelium discoideum cDNA clone VSD160 5', mRNA
sequence.
ACCESSION
AU263574
VERSION
AU263574.1 GI:20522372
KEYWORDS
EST.
SOURCE
Dictyostelium discoideum
ORGANISM
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
1 (bases 1 to 391)
AUTHORS
Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
Unpublished (2002)
JOURNAL
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES
Location/Qualifiers
1. .391
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSD160"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"
ORIGIN
Query Match 1.5%; Score 44.8; DB 9; Length 391;
Best Local Similarity 46.7%; Pred. No. 3;
Matches 136; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 29 TTTCTTCACTTGTTCTCTTATGTTGGTGTATCTCTTAAAAATATAAATCAAAGTCAAAGT 88
Db 386 TTTTNAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAANTAAATTTTANT 327

QY 89 ATATATTTTACAATGAAGTCTCTTTCCCAAGTTTGTATTTTCTACATTTGCTATTTTC 148
Db 326 TTTTAAATTTTTTAAATTTTTTTTTTTTTTTTTTTTTTTCTTTTTCAGTAAATGGT 267

QY 149 CTTTGTCTATGATGCTACCGAGACAGTTTGTGATTCAGAGTGGAGTTCGATGGGAAT 208
Db 266 CTATTTTGGAGATATCTGCTACACCTTTATAGATTGGAATGTTCTTTCAAGAAATCT 207

QY 209 AAAAATGGTAATTTTTTTCAGTTCGTGAGATCGAGAGATCGTGAACCTACCTATTTT 268
Db 206 AAATGTGGGACATTACCATTTCTAAGAGATCAGCAGCAAAATGTAACCAATGATG 147

QY 269 AAGGGAATGTCACTCTAGAAAAATATTTCTGGAAACAGCAGCAGCAATCACA 319
Db 146 TATTCAAGCAACATAAACAATATAAATCAGCCAAAGTGTGAAGAAATTACCA 96
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RESULT 10
AG088699/c
LOCUS
DEFINITION
ACCESSION
VERSION
AG088699.1 GI:16640501
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 592)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Isilam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0245 row: E column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 592.
Location/Qualifiers
1..592
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0245E13"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1..592
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0245E13"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 1.5%; Score 44.6; DB 28; Length 592;
Best Local Similarity 53.8%; Pred. No. 3.5;
Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 62 TTAAATTAATTAATTCAAATCAAGTATATATTTTACAAATGAGTCTCTTCCCAAG 121
Db 433 TTGTAACATATTAATTCGAAATCAGAAAGTATTTGTCTTTAACTTCGTTTCTTTTCAAG 374
QY 122 TTTGTATTTTTCACATTTGCTATTTTCCCTTTGTCTATGATTGCTACCGAGACAGTTTGG 181
Db 373 ATTGTTTTTTTGCCATTTGGAGCCTTGTATGTTCCATATTTATTTTAGAATTACTTTTG 314
QY 182 GATTCAGTGCAGTTTCGATGGGAATAAAATGTAATTTTTCAGTTGCT 232
Db 313 GACTGGAGATATAGCTCAGAGGTAAGAGAACTGACTCCTCTTCTCAAGGT 263

RESULT 12
AG088699
720 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-087L18.F, genomic survey sequence.
AG088699
AG088699.1 GI:16640501
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 720)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
1..720
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-087L18.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 1.5%; Score 44.8; DB 29; Length 720;
Best Local Similarity 55.0%; Pred. No. 3.2;
Matches 88; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 7 TACCTAGTAGAGTTGAGTGAATTTCTTGACTTTGTTTCTCCATTTGGTGTATCTCTTAA 66
Db 311 TATGTAATTTGGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 252
QY 67 ATATTAATTCAAATCAAGTATATATTTTACATGAAGTCTTCTTCCCAAGTTTGT 126
Db 251 AGAGTCATTTGCAGACAAAGTTTAAATGTTGATGTAGTTGATTTCTCAAAATTTTC 192
QY 127 ATTTTCTACATTTGCTATTTTCCCTTTGCTATGATTGCT 166
Db 191 ATTTATGGATCATGTTTGTCTTAATGCTAAGATTGTT 152

RESULT 11
AZ972038/c
LOCUS
DEFINITION
2M0245E13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0245E13 R, genomic survey sequence.
ACCESSION
AZ972038
VERSION
AZ972038.1 GI:13943265
KEYWORDS
SOURCE
Mus musculus (house mouse)

```


Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org
 Request for clones, please contact: Stefan Kappe,
 kappes01@popmail.med.nyu.edu Michael Heidelberger Division,
 Department of Pathology New York University School of Medicine.
 Location/Qualifiers

FEATURES

source

1. .498
 /organism="Plasmodium yoelii"
 /mol_type="mRNA"
 /strain="17XNL"
 /db_xref="taxon:5861"
 /clone="PYCDJ76"
 /dev_stage="sporozoites from salivary gland"
 /lab_host="E. coli TOP10"
 /clone_lib="Plasmodium yoelii sporozoite cDNA"
 /note="Vector: pCR4; TA cloning; Plasmodium yoelii
 sporozoite cDNA library from salivary gland sporozoites 14
 days post-infection"

ORIGIN

Query Match 1.5%; Score 44; DB 12; Length 498;
 Best Local Similarity 56.1%; Pred. No. 4.9;
 Matches 83; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
 QY 15 AGAGGTTGAGTGAATTTCTTGACTGCTTTCTCTATTTGGTGATCTCTTAAATATAA 74
 |||||
 Db 209 AGTGGTCTATTTTATCTTTGATTTTTTTTAGCTCTTCTTACATTTCTTCAATATTTT 150
 |||||
 QY 75 TTCAAAATCAAGTATATATTTTACAAATGAAGTCTTTTCCCAAGTTTGATTTCTTA 134
 |||||
 Db 149 TATCAATATATCTACTTTTTTTTTTTTATTAAGTATTTTTTGTCTAATTCGTTTTTCGT 90
 |||||
 QY 135 CATTTGCTATTTTCCCTTTTGTCTATGAT 162
 |||||
 Db 89 TTATCGTTTCTTATACATTTTCTTTCAT 62
 |||||

Search completed: August 16, 2004, 18:43:21
 Job time : 4920 secs

RESULT 15

BG602721/c

LOCUS

DEFINITION BG602721 Plasmodium yoelii 593 bp mRNA linear EST 14-AUG-2001
 clone PYCDJ76, mRNA sequence.

ACCESSION

BG602721

VERSION

BG602721.1

KEYWORDS

EST.

SOURCE

Plasmodium yoelii

ORGANISM

Plasmodium yoelii

REFERENCE

AUTHORS

Kappe,S.H.I., Gardner,M.J., Brown,S.M., Ross,J., Matuschewski,K.,

Ribeiro,J.M., Adams,J.H., Quackenbush,J., Cho,J., Carucci,D.J.,

Hoffman,S.I. and Nussenzweig,V.

Exploring the transcriptome of the malaria sporozoite stage

Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9895-9900 (2001)

MEDLINE

21396555

PUBMED

11493695

COMMENT

Contact: Malcolm J. Gardner

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301 838 3519

Fax: 301 838 0208

Email: gardner@tigr.org

Request for clones, please contact: Stefan Kappe,

kappes01@popmail.med.nyu.edu Michael Heidelberger Division,

Department of Pathology New York University School of Medicine.
 Location/Qualifiers

FEATURES

source

1. .593
 /organism="Plasmodium yoelii"
 /mol_type="mRNA"
 /strain="17XNL"
 /db_xref="taxon:5861"

/clone="PYCDJ76"

/dev_stage="sporozoites from salivary gland"

/lab_host="E. coli TOP10"

/clone_lib="Plasmodium yoelii sporozoite cDNA"

/note="Vector: pCR4; TA cloning; Plasmodium yoelii

sporozoite cDNA library from salivary gland sporozoites 14

days post-infection"

ORIGIN

Query Match 1.5%; Score 44; DB 12; Length 593;

Best Local Similarity 56.1%; Pred. No. 5;

Matches 83; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 15 AGAGGTTGAGTGAATTTCTTGACTGCTTTCTCTATTTGGTGATCTCTTAAATATAA 74

|||||

Db 209 AGTGGTCTATTTTATCTTTGATTTTTTTTAGCTCTTCTTACATTTCTTCAATATTTT 150

|||||

QY 75 TTCAAAATCAAGTATATATTTTACAAATGAAGTCTTTTCCCAAGTTTGATTTCTTA 134

|||||

Db 149 TATCAATATATCTACTTTTTTTTTTTTATTAAGTATTTTTTGTCTAATTCGTTTTTCGT 90

|||||

QY 135 CATTTGCTATTTTCCCTTTTGTCTATGAT 162

|||||

Db 89 TTATCGTTTCTTATACATTTTCTTTCAT 62

|||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: August 16, 2004, 07:10:13 ; Search time 7610 Seconds
(without alignments)
17086.610 Million cell updates/sec

Title: US-09-428-122-1
Perfect score: 3000
Sequence: 1 cgccttaactagtagaggt.....tgcttgctaaacactttc 3000

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_hg_hum.*

31: em_hg_inv.*

32: em_hg_other.*

33: em_hg_mus.*

34: em_hg_pln.*

35: em_hg_rod.*

36: em_hg_mam.*

37: em_hg_vrt.*

38: em_sy.*

39: em_higo_hum.*

40: em_higo_mus.*

41: em_higo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description	
		Match	Length				
1	3000	100.0	3000	6	BD261378	Chlamydia	
2	2988	99.6	16448	1	AE001587	Chlamydia	
3	2988	99.6	26920	1	CPN133035	Chlamydia	
C	4	2986.4	99.5	12127	1	AE002235	Chlamydia
	5	2986.4	99.5	299650	1	AP002545	Chlamydia
	6	2984.8	99.5	300923	1	AE017157	Chlamydia
	7	2975.4	99.2	110000	6	AR310754_00	Sequence 9
	8	2775.8	92.5	2787	6	A81835	Sequence 9
9	2775.8	92.5	2787	6	BD192261	Surface e	
10	2241	74.7	2241	6	AX349497	Sequence	
C	11	570.4	19.0	300512	1	AE016995	Chlamydia
	12	546.6	18.2	2781	6	AX662119	Sequence
	13	546.6	18.2	2781	6	AX666191	Sequence
14	546.6	18.2	4926	1	CPU72499	U72499 Chlamydia	
C	15	533.2	17.8	300380	1	AE017158	Chlamydia
16	531.8	17.7	12676	1	AE002192	Chlamydia	
C	17	531.8	17.7	300650	1	AP002546	Chlamydia
C	18	531.2	17.7	10757	1	AE001628	Chlamydia
19	530.2	17.7	2815	6	A81829	Sequence 3	
20	530.2	17.7	2815	6	BD192258	Surface e	
C	21	530.2	17.7	17280	1	CPN133034	Chlamydia
22	527	17.6	2787	6	AX349573	Sequence	
23	524.6	17.5	2957	6	BD244667	Chlamydia	
24	523	17.4	534	6	AX349495	Sequence	
25	522.2	17.4	2757	6	A81837	Sequence 11	
26	522.2	17.4	2757	6	BD192262	Surface e	
27	520	17.3	300380	1	AE017158	Chlamydia	
C	28	518.4	17.3	10026	1	AE002193	Chlamydia
	29	518.4	17.3	110000	6	AR310754_05	Continuation (6 of
	30	518.4	17.3	300650	1	AP002546	Chlamydia
	31	518.2	17.3	2950	6	BD261385	Chlamydia
	32	516.6	17.2	2787	6	AX349511	Sequence
33	516.6	17.2	10757	1	AE001628	Chlamydia	
34	516.6	17.2	17280	1	CPN133034	Chlamydia	
35	515.2	17.2	2784	6	BD261386	Chlamydia	
36	515.2	17.2	15068	1	AE001627	Chlamydia	
37	515	17.2	2787	6	A81839	Sequence 13	
38	515	17.2	2787	6	BD192263	Surface e	
C	39	515	17.2	12676	1	AE002192	Chlamydia
	40	514	17.1	2793	6	A81841	Sequence 15
	41	514	17.1	2793	6	AX349523	Sequence
42	514	17.1	2793	6	BD192264	Surface e	
43	513.6	17.1	3000	6	BD261387	Chlamydia	
44	512.6	17.1	2950	6	BD261383	Chlamydia	
C	45	509.8	17.0	110000	6	AR310754_05	Continuation (6 of

ALIGNMENTS

RESULT 1	BD261378	3000 bp	DNA	linear	PR 17-JUL-2003
LOCUS	Chlamydia antigens and corresponding DNA fragments and uses				
DEFINITION	thereof				
ACCESSION	BD261378				
VERSION	BD261378.1	GI:33071146			
KEYWORDS	JP 2002528111-A/1.				
SOURCE	Chlamydia pneumoniae				
ORGANISM	Chlamydia pneumoniae				
REFERENCE	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia				
AUTHORS	1 (bases 1 to 3000)				
TITLE	Murdin,A.D., Oomen,R.P. and Dunn,P.L.				
JOURNAL	Chlamydia antigens and corresponding DNA fragments and uses thereof				
	Patent: JP 2002528111-A 1 03-SEP-2002;				

Pred. No. is the number of results predicted by chance to have a

QY	1741	GCTCAAAGCTTCTGGAACCTGTTAAACAGACCCGAGTGA	CTCCAGATCTCTATATATGGGTGA	1800
Db	1741	GCTCAAAGCTTCTGGAACCTGTTAAACAGACCCGAGTGA	CTCCAGATCTCTATATATGGGTGA	1800
QY	1801	GAATTTCCATTAGCGGTATACAGGAACTTGGGCGCCAAATGTTTGGGGACACGGGCTTC		1860
Db	1801	GAATTTCCATTAGCGGTATACAGGAACTTGGGCGCCAAATGTTTGGGGACACGGGCTTC		1860
QY	1861	TAGGACTGCAACCTTCAACTGGAATAAACTGCTATATTCCTAAATCCCGAGGATACGG		1920
Db	1861	TAGGACTGCAACCTTCAACTGGAATAAACTGCTATATTCCTAAATCCCGAGGATACGG		1920
QY	1921	CTCTTTAGTCCCTAATAGCTATATGATGATATATAGCTCTCTCCATTATCT		1980
Db	1921	CTCTTTAGTCCCTAATAGCTATATGATGATATATAGCTCTCTCCATTATCT		1980
QY	1981	TATGGAGACTGCAAAACCAAGGGTTGACGAGACCGTGCTTTTGGTGTGCTCGATTATC		2040
Db	1981	TATGGAGACTGCAAAACCAAGGGTTGACGAGACCGTGCTTTTGGTGTGCTCGATTATC		2040
QY	2041	TAACTTCTTCCATAAGGATAGTACAAAAACACGACGGGGTTTCGCCATTGAGTGGCGG		2100
Db	2041	TAACTTCTTCCATAAGGATAGTACAAAAACACGACGGGGTTTCGCCATTGAGTGGCGG		2100
QY	2101	TTATGTCATAGGAGAACTTACATACCTGTTGTCAGATAAGATCTTCTAGTGTGCTGATTTG		2160
Db	2101	TTATGTCATAGGAGAACTTACATACCTGTTGTCAGATAAGATCTTCTAGTGTGCTGATTTG		2160
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Db	2161	TCAGCTCTTTGGAGACATAGAGACTACTTTGTAGCTAAGAAATCAAGTACAGTCTACGG		2220
QY	2221	AGGAACTCTCTATTAACGAGCAACACGAAACCTATATCTCTCTTCTGCAAACTACGGCC		2280
Db	2221	AGGAACTCTCTATTAACGAGCAACACGAAACCTATATCTCTCTTCTGCAAACTACGGCC		2280
QY	2281	TTGTTGCTGCTTATGTTCTCAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTA		2340
Db	2281	TTGTTGCTGCTTATGTTCTCAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTA		2340
QY	2341	CACCCATACGGAATACGATCTGMAAACCAAGTATACAAATATCTCTGTTTAAAGGAAG		2400
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QY	2401	CTGGGGGAATGATAGTTTCGCTTTAGAAATCGTGGAAGAGCGTCGGATTGCTTAGATGA		2460
Db	2401	CTGGGGGAATGATAGTTTCGCTTTAGAAATCGTGGAAGAGCGTCGGATTGCTTAGATGA		2460
QY	2461	AAGTGCTCTATTGACGAGTACATGCCCTTCATGAAATTCAGATTGTCATGCAATCA		2520
Db	2461	AAGTGCTCTATTGACGAGTACATGCCCTTCATGAAATTCAGATTGTCATGCAATCA		2520
QY	2521	GGAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTAGCCGCTTTGTGAA		2580
Db	2521	GGAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTAGCCGCTTTGTGAA		2580
QY	2581	TCTTCCCTTACTATCGGATCCGATTTGATGAAGAAATCAGACTCGCAAGATGCAACGTA		2640
Db	2581	TCTTCCCTTACTATCGGATCCGATTTGATGAAGAAATCAGACTCGCAAGATGCAACGTA		2640
QY	2641	CAATCTAATCTTGTGTTATCTGTTAGTAAACCTTCGGTACGAAATTTGGCAAGCAAGCTTT		2700
Db	2641	CAATCTAATCTTGTGTTATCTGTTAGTAAACCTTCGGTACGAAATTTGGCAAGCAAGCTTT		2700
QY	2701	ACTGCGAAATAGCGGTGATCTTTGAAAAACCTTCGGTACGAAATTTGGCAAGCAAGCTTT		2760
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QY	2761	AGTCCTCTCGGAGGAAACATTTTGTCTTTTAACTCAAAATTTTGAAGCCCTTAGCCAAAT		2820
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LOCUS				
DEFINITION				
Chlamydia pneumoniae section 3 of 103 of the complete genome.				
ACCESSION				
AE001587 AE001587.1				
VERSION				
AE001587.1 GI:4376271				
KEYWORDS				
SOURCE				
ORGANISM				
Chlamydia pneumoniae CWL029				
REFERENCE				
1 (bases 1 to 16448)				
AUTHORS				
Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R.W.,				
Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.				
TITLE				
Comparative genomes of Chlamydia pneumoniae and C. trachomatis				
JOURNAL				
Nat. Genet. 21 (4), 385-389 (1999)				
MEDLINE				
99206606				
PUBMED				
1019388				
REFERENCE				
2 (bases 1 to 16448)				
AUTHORS				
Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L.,				
Grimwood, J., Davis, R.W. and Stephens, R.S.				
TITLE				
Direct Submission				
JOURNAL				
Submitted (01-DEC-1998) Program in Infectious Diseases, University				
of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA				
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1. 16448				
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CDS				

QY	1261	TGATCCCAATACACAGATCATCCAAACAGTTACAGATGTCCTTAAAGTTAATGAGAC	1320
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QY	1321	TCCGGCAGATTCGACATCAATATACAGGAACATCATCTTACAGGAGAAAGTTATC	1380
Db	18981	TCCGGCAGATTCGACATCAATATACAGGAGAAATCATCTTACAGGAGAAAGTTATC	19040
QY	1381	AGAGACAGAGCCCGCAGATTCTAAAAATCTTACTTGAAGCTACTACAGCCTGTAACTCT	1440
Db	19041	AGAGACAGAGCCCGCAGATTCTAAAAATCTTACTTGAAGCTACTACAGCCTGTAACTCT	19100
QY	1441	TTCAGAGGTACTCTATCTTTTAAACATGAGTGACTCTCAGACTCAGGCATTCACATCA	1500
Db	19101	TTCAGAGGTACTCTATCTTTTAAACATGAGTGACTCTCAGACTCAGGCATTCACATCA	19160
QY	1501	ACAGGCAGATTCCTGCTCTGAAATGAGCTAGGAATCTACTCTAGAACCTCTGATACTAG	1560
Db	19161	ACAGGCAGATTCCTGCTCTGAAATGAGCTAGGAATCTACTCTAGAACCTCTGATACTAG	19220
QY	1561	CACCATAAACAAATTTGGTCAATTAACATCAGTTCTTATAGACGGTGCAAGAGCAAAAAT	1620
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QY	1621	AGAAACCAAGCTACGTCAAAAATCTGACTTTATCTGGAACCATCACTTTATTGGACCC	1680
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QY	1681	GACGGCAGCTTTTATGAATCATAGTTTAAAGATCTCAGTCTCTACGATCTTAGA	1740
Db	19341	GACGGCAGCTTTTATGAATCATAGTTTAAAGATCTCAGTCTCTACGATCTTAGA	19400
QY	1741	GCTCAAAGCTTCGGAACGTAAACAGCAGCGAGTCACTCCAGATCTTATAGTGTGA	1800
Db	19401	GCTCAAAGCTTCGGAACGTAAACAGCAGCGAGTCACTCCAGATCTTATAGTGTGA	19460
QY	1801	GAAATTCATACGGCTATCAGGAACTTTGGGGCCCAATGTTTGGGGACAGGGGCTTC	1860
Db	19461	GAAATTCATACGGCTATCAGGAACTTTGGGGCCCAATGTTTGGGGACAGGGGCTTC	19520
QY	1861	TACGACTGCAACTTCAACTGACTAAAACTGGCTATATTCCTTAATCCCGAGGATCG	1920
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QY	1921	CTCTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGCTCTCCATTATCT	1980
Db	19581	CTCTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGCTCTCCATTATCT	19640
QY	1981	TATGAGACTCAAAAGAGGTTGAGGAGACCGTGTCTTTGGTGTGCTGGATATC	2040
Db	19641	TATGAGACTCAAAAGAGGTTGAGGAGACCGTGTCTTTGGTGTGCTGGATATC	19700
QY	2041	TAACTCTTCCATAAGGATAGTACAAAAACAGACGCGGTTTCGCATTTGAGTGGCG	2100
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QY	2101	TTATGTATAGAGGAAACCTACATCTTTGTCAGATAAGATTTCTAGTGTGCAATTTG	2160
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Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39			
Nucleic Acids Res. 28 (6), 1397-1406 (2000)			
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.

1 Shirai, M., Hirakawa, H., Ouchi, K., Tabuchi, M., Kishi, F., Kimoto, M., Takeuchi, A., Nishida, J., Shibata, K., Fujinaga, R., Yoneda, H., Matsushima, H., Tanaka, C., Furukawa, S., Miura, K., Nakazawa, A., Ishii, K., Shiba, T., Hattori, M., Kuhata, S. and Nakazawa, T.
Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of Chlamydia pneumoniae isolates from Japan and the United States
J. Infect. Dis. 181 Suppl 3, S524-S527 (2000)
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2 Shirai, M., Hirakawa, H., Kimoto, M., Tabuchi, M., Kishi, F., Ouchi, K., Shiba, T., Ishii, K., Hattori, M., Kuhara, S. and Nakazawa, T.
Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA
Nucleic Acids Res. 28 (12), 2311-2314 (2000)
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3 (bases 1 to 299650)
Shirai, M.
Direct Submission
Submitted (04-JUL-2000) Mutsunori Shirai, Yamaguchi University School of Medicine, Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi 755-8505, Japan
(E-mail: mshirai@po.cc.yamaguchi-u.ac.jp, Tel: 81-836-22-2227, Fax: 81-836-22-2415)
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AUTHORS Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomydia.
Geng,M.M., Schuhmacher,A., Muehldorfer,I., Bensch,K.W.,
Schaefer,K.P., Schneider,S., Pohl,T., Essig,A., Marre,R. and
Melchers,K.
The genome sequence of Chlamydia pneumoniae TW183 and comparison
with other Chlamydia strains based on whole genome sequence
analysis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 300923)
AUTHORS Geng,M.M., Schuhmacher,A., Muehldorfer,I., Bensch,K.W.,
Schaefer,K.P., Schneider,S., Pohl,T. and Melchers,K.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2002) RDR/IT, RDR/FG, RDR/BT, ALTANA Pharma,
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ACCESSION BD192261
VERSION BD192261.1 GI:33002000
KEYWORDS JP 2002510970-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2787)
AUTHORS Birkelund,S., Christiansen,G., Knudsen,K., Madsen,A.S. and
Mygind,P.
TITLE Surface exposed proteins from chlamydia pneumoniae
JOURNAL Patent: JP 2002510970-A 5 09-APR-2002;
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PR 23-JUN-1997 DK 0744/97
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PI MADSEN,
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VERSION AE016995.1 GI:29834389
KEYWORDS

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FEATURES
source

Chlamydomophila caviae GPIC
Chlamydomophila caviae GPIC
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
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Umayam,L.A., Haft,D.H., Peterson,J., Beanan,M.J., White,O.,
Saizberg,S.L., Hsia,R.C., McClarty,G., Rank,R., Bavoil,P. and Fraser,C.
Praser,C.M.
Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
examining the role of niche-specific genes in the evolution of the
Chlamydiaceae
Nucleic Acids Res. 31 (8), 2134-2147 (2003)
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2 (bases 1 to 300512)
Read,T., Myers,G., Brunham,R., Nelson,W., Paulsen,I.,
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Hsia,R.-C., McClarty,G., Rank,R., Bavoil,P. and Fraser,C.
Direct Submission
Submitted (29-OCT-2002) The Institute for Genomic Research, 9712
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QY	671	ACCTCCTCAAGAAAGGGAGGCCATTCAGATTCGATCCCTTACCATTAATCTGGAAC	730	QY	1745	AAAGCTTCTGGAATCTTAACAGACCGCAGTGACTCCAGATCTCTATATATGAGGTGAGAA	1804
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QY	731	CAAGGGAGTCTCTTTTCTGACAAATCTTCTTGGATTCTGGAGCTGCAATTTTACA	790	QY	1805	TTCCATTACGGCTATC-AGGAACTTGGGGCCCAATTTGTTGGGGACAGGGGCTTCTAC	1863
Db	23987	CAAGGAAGTCAATTTTCTGGAATACTGCGGTGAATTTCTGGAGGACGATATGCA	23928	Db	22937	CAACATTTATGGGTATCAAGGAACTGGTCTCTCTGGATTACAGATAACGGCTCAGAT	22878
QY	791	GAAGCTCGGTGACTTATTTCTTAATTAATGCTAAAGTTTCTTTATTTGACAATAAGTTCACA	850	QY	1864	G-----ACTGCAACCTTCAACTGGACTAAACTGGCTATATTCCTAATCCGAG	1912
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QY	851	GGAGCGAGCTCTCAACAACGGGGATATGTCAGGAGGTGCTATCTGTCTTATAAACT	910	QY	1913	CGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGCTCTCTC	1972
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QY	1031	ACCTTATTCAGTAGAAATAGTCTCAATGAGGTAGAGCTCTTAAAGTGGAGCCATAGCT	1090	QY	2090	TTGAGTGGCGGTATGTCTATAGGAGAAACCTTACATCTTGTTCAGATAAGATTTCTAGT	2149
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Db	23465	ATAGTTGTTGG-----GGTACTGTGCGAGATCTTCTCACTTTAAACCAAGCT	23418	Db	22397	GATGCGCAAGTTTACCTATTGCCATACCAACAACAACATGACCAACGCTTATACAGATT	22338
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QY	1388	GAGGCGGAGATTTCAAAATCTTACTTCAAGAGTACTACAGCTCTTAATCTTTTCAGGA	1447	QY	2444	CCGATTTGCTTAGATGAAAGTCTCTATTGAGCAGTACATGCCCTTCAATGAAATGCGAG	2503
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QY	1448	GGTACTCTATCTTTAAACATGGAGTACTCTGCACTCAGGACTCAGGCAATTCCTCAACAGGCA	1507	QY	2504	TTTGTCTATGCAATCAGAGAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGA	2563
Db	23297	GGAGAGCTTATCTTAAGAAACCGTGTGGAAGTAGAGGCAAAAGCTGTTTCGCAACAGCG	23238	Db	22217	GTGTCTATGCTCATCAAGAGGATTTTAAAGAACCTTCAAGAGAGGCGGCTACCTTTGAA	22158
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Db	23237	GGCTCTCTAATTTGATGATGAGGAAACAAGAGTGTCTGCAAAACAGAGATGTCAGC	23178	Db	22157	AGTAGGATCTTCTCAATGTTTCCGTCCTATAGGCGTGAAGTTTGAGAAACTCGTCTAC	22098
QY	1565	ATAAACAATTTGGTCTAATTAACATCAGTTCTATAGACGGTGGCAAGAGGCAAAATAGAA	1624	QY	2624	TGCCAAGATGCAACGTACAACTAATCTTGTGTTATCTGTTGATCTTCTTGTAGTAAC	2683
Db	23177	CTAACCAACCTGGGATCAATCTTAATTTTATAGTGGAAACAAATCGCTGTTATTGCC	23118	Db	22097	GGAGAAAAAAGCTGTTATGATCTTACATTTGATGTTATCTTCCGTGATGTGTACCGTCAAT	22038
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RESULT 12
AX662119 2781 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 56 from Patent WO02053588.
ACCESSION AX662119
VERSION AX662119.1 GI:29163057
KEYWORDS Chlamydomophila psittaci
SOURCE Chlamydomophila psittaci
ORGANISM Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
REFERENCE 1
AUTHORS Johnston,S.A., Stenke-Hale,K., Sykes,K.F. and Kaltenboeck,B.
TITLE Methods and compositions for vaccination comprising nucleic acid
and/or polypeptide sequences of chlamydia psittaci
JOURNAL Patent: WO 02053588-A 56 11-JUL-2002;
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
FEATURES
Location/Qualifiers
source 1..2781
/organism="Chlamydomophila psittaci"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 18.2%; Score 546.6; DB 6; Length 2781;
Best Local Similarity 53.7%; Pred. No. 3.7e-117;
Matches 1390; Conservative 0; Mismatches 1134; Indels 63; Gaps 10;

Qy 328 TTTTAAACAACACTAAGCGGATTTGACTTTCACAGGTAAAGGGAACCTCTATTGTCCA 387
Db 231 TTTTGTTCAGACTGCACACACCTAACTTTCAAGAGGGAACACCTAGCTTATCCATAAC 290
Qy 388 AACGGTGGATGACGGGACTGTAGCAGGGGTGCTGTTTAAACAGCAGCGGTGTAGATAATC 447
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Qy 448 TACCACGTTATAGGGTTTTCGCTACTTTTATTCGCTCTCCTCGAAGTTCGATAAC 507
Db 348 TCTTACCGCTCACAGATTTTCTAAGTTGAGCTTTTAAAGAAATGCCCATCTTCTCTAGTGA 407
Qy 508 TACCGCAAAAGGAGCCGTAGCTCTCTACGGTAGCTTGAGTTTGACAAAATATGTCAG 567
Db 408 TACTGGAAGAGGGC---TATGAATCCGAGGAGCAATAAATTAGGGAATATGCGAG 464
Qy 568 TTTGCTCTTCAGCAAAAACCTTTTCAACGGATAATGGCGGTGCTATCACCGCAAAAACCTCT 627
Db 465 TATTCTGTTGATCAGAATATTCCGCTGAGAATGGTGAGCCATCTCTTGCAAGCTTT 524
Qy 628 TTCATTAAACAGGACTCAATGTAGCTCTGTTTCTGGAATACTCTCTCAAGAAAGG 687
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Qy 688 CGGAGCCATTACAGATCTCCGATGCCCTTACCATTACTGGAACCAAGGGAAGTCTCTTT 747
Db 585 TGGAGCGAATTCGCTGCTAGGGAATAGCTCATCTTTTCGCAACCAAGGCAATCAGATT 644
Qy 748 TTTGCAAACTACTTCTTCGGAATCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTAT 807
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Qy 868 AACGGGGATATGTACAGAGGTGCTATCTGTGCTTATAAAAACCTAGTACAGATACTAAGGT 927
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Qy	1930	CCCTAA	TAGCTT	ATGGAA	TGCAT	TATTA	PAGATA	TAT	TAGCT	CTCT	CCAT	TAT	CTTAT	TGAGAC	1989															
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Qy	1990	TGCAAA	CGAA	GGGT	TGC	---	AGG	GAG	ACCG	TGCT	TTTTT	TG	TG	TGCT	GTG	CTG	CGAT	TAT	TAACTT	2046										
Db	1875	TAGT	TTT	GAT	AGT	TAT	CTT	TG	AG	AC	CGT	CTG	TGG	TTT	TG	TG	TGG	CTCT	TG	GAAT	TTG	GGAAC	CTT	1934						
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Qy	2107	CATAG	GAG	GAAC	CC	TAC	AT	CTT	CT	TC	TC	CAG	AT	A	AG	AT	CTT	TAG	TG	CT	GC	AT	TTTT	TG	CAGCT	2166				
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Qy	2227	TCTCT	AT	T	ACC	G	CA	---	---	CA	AG	GA	CC	T	AT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CGGC	2280		
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Qy	2281	TTGTT	TC	T	TG	TAT	GT	CT	CT	C	A	G	A	GT	TC	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	2340		
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Qy	2341	CACCA	TAC	CG	GA	TAA	CC	AT	CT	GA	AA	CC	AG	TAT	AC	AA	TAT	CC	TACT	CT	CT	CT	CT	CT	CT	CT	CT	2400		
Db	2235	TTGCC	AC	CG	CC	CA	AC	AT	GA	CA	CG	CT	CT	AT	AC	AG	CT	AT	CT	CT	CT	CT	CT	CT	CT	CT	CT	2294		
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Db	2355	TTCT	T	CT	CT	TTG	AT	AG	TT	TAT	G	CA	CG	TT	TG	CA	AA	AA	TT	CA	AG	TT	TG	CT	CT	AT	TG	CA	2414	
Qy	2521	GGA	AG	GT	TT	T	AA	GA	CA	GG	GA	C	AG	AG	CT	CG	T	GA	AT	TT	G	GA	AG	TAG	CG	CT	TG	GA	2580	
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RESULT 13	AX666191	2781 bp	DNA	linear	PAT 26-MAR-2003
LOCUS	AX666191	2781 bp	DNA	linear	PAT 26-MAR-2003
DEFINITION	Sequence 56 from Patent WO0247718.				
ACCESSION	AX666191				
VERSION	AX666191.1	GI:29209994			
KEYWORDS	Chlamydomophila psittaci				
SOURCE	Chlamydomophila psittaci				
ORGANISM	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.				
REFERENCE	1 Johnston, S.A.				
AUTHORS	Methods and compositions for vaccination comprising nucleic acid				
TITLE	ad/or polypeptide sequences of i(chlamydia)				
JOURNAL	Patent: WO 0247718-A 56 20-JUN-2002;				
	BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)				
FEATURES	Location/Qualifiers				
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psittaci
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4926)
AUTHORS Longbottom, D.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-1996) Moredun Research Institute, 408 Gilmerton
        Road, Edinburgh EH17 7JH, Scotland, UK
FEATURES
    Location/Qualifiers
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Run on: August 16, 2004, 15:10:08 ; Search time 153 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	509.8	17.0	1230025	US-09-198-452A-1	Sequence 1, Appli
3	243.4	8.1	3150	US-09-430-723-1	Sequence 1, Appli
4	140.6	4.7	3354	US-09-612-402B-23	Sequence 23, Appli
5	133.8	4.5	3324	US-09-612-402B-24	Sequence 24, Appli
6	132.2	4.4	3021	US-09-556-877-182	Sequence 182, App
7	132.2	4.4	3021	US-09-620-412C-182	Sequence 182, App
8	132.2	4.4	3021	US-09-598-419-182	Sequence 1, Appli
9	132.2	4.4	4435	US-09-612-402B-1	Sequence 170, App
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16	50.6	1.7	2643	US-09-620-412C-169	Sequence 169, App
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18	50.4	1.7	1511	US-09-612-402B-10	Sequence 10, Appli
19	50.4	1.7	1515	US-09-612-402B-22	Sequence 22, Appli
20	50.2	1.7	2601	US-09-556-877-181	Sequence 181, App
21	50.2	1.7	2601	US-09-620-412C-181	Sequence 181, App
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23	42.6	1.4	832	US-09-621-976-2813	Sequence 2813, App
24	42.4	1.4	474	US-09-621-976-18033	Sequence 18033, A
25	42.4	1.4	6124	US-08-213-419B-3	Sequence 3, Appli
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27	39	1.3	1896	US-09-620-412C-324	Sequence 324, App

28	39	1.3	1896	4	US-09-598-419-324	Sequence 324, App
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32	37.6	1.3	2076	4	US-09-598-419-312	Sequence 312, App
33	37.6	1.3	5265	4	US-09-556-877-174	Sequence 174, App
34	37.6	1.3	5265	4	US-09-620-412C-174	Sequence 174, App
35	37.6	1.3	5265	4	US-09-598-419-174	Sequence 174, App
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37	36.8	1.2	1269	3	US-09-107-858-11	Sequence 11, Appli
38	36.8	1.2	1269	4	US-09-579-174-11	Sequence 94, Appli
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41	36	1.2	2547	4	US-09-620-412C-184	Sequence 184, App
42	36	1.2	2547	4	US-09-598-419-184	Sequence 184, App
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45	36	1.2	2895	4	US-09-598-419-171	Sequence 171, App

C

ALIGNMENTS

RESULT 1

US-09-198-452A-1

; Sequence 1, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 1

; LENGTH: 1230025

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

; FEATURE:

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Matches 2998; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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DB 31718 CTTTAAATATTAATTCAAAATCAAAGTATATATTTTAAATGAAGTCTTTTCCCAA 31777
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QY 901 TTAATAAACTAGTACAGATACTAAGGTTCACCCCTCACTGGAAATCAGATGTTACTTTCAG 960
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QY 1081 AGCCATAGCTATCGAAGATAGTGGGAAATTTAGTTTATCGCCGCAATAGAGTAGTATCGACTT 1140
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QY 1141 CTTTTTAGGAATACAGTCACTTCTACTACTCTCTGGACGAATAGAGTAGTATCGACTT 1200
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US-09-198-452A-1/c

US-09-198-452A-17C
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Best Local Similarity 52.7%; Pred. No. 2.2e-142;

Matches 1410; Conservative 0; Mismatches 184; Indels 81; Gaps 11;

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Qy 307 CACAGCAATCAGAAAAGCTGTTTAAACACACTAAGGGGATTTGACITTCACAGGTAA 366
Db 517986 --CAGCTTTAACGAAGGGTTGTTTTCTGACACTACGGAATCTTTAAGCTTTTCCCGGTAA 517929

Qy 367 CGGGAACCTCTATTGTTCCAAACGGTGGATGCAGGACTGTAGAGGGGCTGCTGTATA 426
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; Patent No. 6607730
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; APPLICANT: Murdin, Andrew
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 19721-011
; CURRENT APPLICATION NUMBER: US/09/430,723
; CURRENT FILING DATE: 1999-10-29
; EARLIER APPLICATION NUMBER: 60/106,590
; EARLIER FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/133,071
; EARLIER FILING DATE: 1999-05-07
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US-09-430-723-1

Query Match 8.1%; Score 243.4; DB 4; Length 3150;
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Qy 1094 GAAGATAGTGGGAAATTTAGTTTATCCGCGATAGTGGTACACATTTGCTTTTATAGGGAAT 1153
Db 1244 CCGGAATCTGGGAGCTCTCTATCCGAAATCAAGGTGATATCTCTTTTAAACAAGAC 1303
Qy 1154 ACAGTCACTTCTACTCTCTCGGAGCAATAGAGTAGTATCGACTTAGGAACGAGTGCA 1213
Db 1304 C---TCAGCATCACTAGTGGGACACCTACTCGCAATAGTATTCACTTCGGAAGAATGCC 1360
Qy 1214 AAGATGACAGCTTTGGCTTCTGCTGTGGTGGAGCCATCTACTTATGATGCCATAACT 1273
Db 1361 AAGTTTGCCACTCTAGGGAATAGCAAGGCTATACCCCTATCTTCTATGATCGGATTACA 1420
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Qy 1274 ACAGGATCATCCCAACAGTTACAGATGTCTTAAAGCTTAATGAGACTCCGCGAGATTCT 1333
Db 1421 TCTGATGATTTATCTGTGTCATCCGACGCGCTACTGTGTGTCATTCATCCAAACCGCAGT 1480
Qy 1334 GCA---CTACAATATACAGGGAACATCATCTTACAGGAGAAAAGTTTATCAGACACAGAG 1390
Db 1481 GCAGATGGTGGTATTCAGGGACTATTTGTTCTTTTCAGGAGAAACCCCTCACTGCTACCGAA 1540
Qy 1391 GCCGCGATTTCTAAAATCTTACTTGAAGCTACTACAGCTGTGTAATCTTTTCAGGAGGT 1450
Db 1541 GCAGCAACCCCTGCAAAATGCTACATCTACATTTAAACCAAAAGCTTAGAACTTTGAAGCGGT 1600
Qy 1451 ACTCTATTTTAAAACATGAGTGTCTCTCGACACTCAGGCATTCATCTAACAGGCGAGAT 1510
Db 1601 ACTCTGCTTTTAAAGAACGGTGTCTACTTAAATGTTTCATTAACCTTCACGCAAGATGAAAG 1660
Qy 1511 TCTCGTCTCGAAATGGACGTAGGAATCTACTCTAGAACCTCTGTGATA----- 1556
Db 1661 TCGTCTCATCATGATGATGACGGACCACTTAGCACTACAAATGGAGCTAATAATACT 1720
Qy 1557 -----CTAGACCATATAACAATTTGGTTCATTTAAACATCAGTTCTATAGACGGTGCAAG 1609
Db 1721 GACGGTCTATCACCTTAAACAAGCTTGTAAATCAATCTGGAATCTTTGGATGGCACTAAA 1780
Qy 1610 AAGGCAAAATAGAACCAACCAAGCTACGTCAAAAATCTGACTTTTCTGCAACCATCACT 1669
Db 1781 GCGGCTGTCTTAATGTGCAGATACCAATGGAGCTCTCACTATATCCGGAACCTTTAGGA 1840
Qy 1670 TTATTGGACCCGACGGGACGTTTATGAAAATCATAGTTTAAAGAAATCCTCAGTCTCTAC 1729
Db 1841 CTTGTGAAAACCTCTCAAGATTCTGTGCAACCAACGGGATGTTTAAATAAGATTTCACG 1900
Qy 1730 GAC-----ATCTTAGAGCTCAAAGCTTCTGGA---ACTGTAAACAACACCGCAGTCACT 1780
Db 1901 CAAAGTCCGATTTTAGAACTCAAAGCGACTTCAAATACTGTAACTACTAACCACTACGGACTTCAGT 1960
Qy 1781 CCAGATCCTATATGTTGGTGAATAATTCATTAAGGCTATCAGGCTATCAGGGAATCTGGGCCCCAATT 1840
Db 1961 CTCGGCACAAACCGGCTATCAGCAATCTCCCTATGGGTATCAAGGAACCTTGGGAGTTTACC 2020
Qy 1841 GTTTGGGGAGACGGGCTTCTACGACTGCAACCTTCAAATGGGACTAAACCTGGGTATATT 1900
Db 2021 ATAGACACGACAAACCATACGGTCAAGGA-----AATTGGAAAACCAACCGGTTATCTT 2074
Qy 1901 CTTAATCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCATTTATAGAT 1960
Db 2075 CCTCATCCGAGCGCTCTTGTCCCTCATTTCTTAATAGCCTATATGGGCAACCGTCATAGAT 2134
Qy 1961 ATTAGCTCTCTCCATTTCTTATGGAGACTGCAACGAAAGGTTGCGAGGAGACCGTGCT 2020
Db 2135 TTACGAGCTGTAAAGTCAAGGTCAAGCTGATGGCGAAGATGTCCCTGGGAGAAC-- 2192
Qy 2021 TTTTGTGTGCTGGATTTATCTTAATCTTCTTCCATAAGGATAGTACAAAAACACACACGCGG 2080
Db 2193 -TGAGCATCACAGGAATTACAATTTCTCCATCGCAATCATACCGGTGATGACGACG 2251
Qy 2081 TTTTGGCAATTTAGTGGCGGTTTATGTCATAGGAGGAAACCTACATCTTGTTCAGATAAG 2140
Db 2252 TACCGCATATGGTGGAGGCTACCTCATCAATACCTACACGCGCATCACTCCAGATGCT 2311
Qy 2141 ATTTCTTAGTGTGCTATTTGTGCTGCTCTTTGGAGAGATAGAGACTACTTTGTAGCTAAG 2200
Db 2312 GCGTTAAGTCTAGTTTGGACAGCTGTTTACAAAATCTAAGGATTAACCTCGTAGGTAC 2371
Qy 2201 AATCAAGGTACAGTCTACGAGGAACTCTCTATTTACGACCAACCAACCTATATCTCT 2260
Db 2372 GGTCAATCTTAAAGTTTATTTTCGTACAGTATACTCTAAATC----- 2413
Qy 2261 CTTTCTTGCAAACTACCGGCTTTGTTGTTGTCTTATGTTTCTTACAGAGATTCTGTCTTC 2320
Db 2414 -----ACCAAGTCTCTGTTTGGATCATCGAGATTCTTCTCAGGAGGACCTTCTC 2462
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QY 2321 TTTTCAGGAACCTTTAGCTACACCATACGATACGATCTGAAACCAAGTATATCAACA 2380
Db 2463 GAG-----TTACCTATAGCGGTAGCAATGAGAAAGTAAAGACTTCATATACAAA 2512
QY 2381 TATCCTACTGTTAAAGGAGCTGGGGGATGATAGTTTCGCTTTTGAATTCGGTGAAGA 2440
Db 2513 TTGCCATAAGGCGCTGCTCTCTGGAGTAAACAAATGCTGGTTAGGAGAACTCGAAGGGAAC 2572
QY 2441 GCTCCGATTTGCTTAGATGAAAGTCTCTA---TTTGAGCAGTACATGCCCCCTTCATGAAA 2497
Db 2573 CTTCCATCACTCTCTCTCTCGCATCTTAACCTCAAGCAGATCATTCCTCTTGTAAAA 2632
QY 2498 TTGCAGTTTGCTATGCAATCAGGAAGTTTTAAAGAACAGGGAACAGAGCTCGTGAA 2557
Db 2633 GCTGAAGTTGCTTACGCGACTCATGGGGGCATCCAAAGAAAATACCCCGAGGGGAGATT 2692
QY 2558 TTTGGAAGTAGCGCTCTGTGATCTTGCCTTACCTATCGGATCCGATTCGATATAGGAA 2617
Db 2693 TTTGACACGGTCACTACTCAACGTGCGAGTTCCCGTAGGGCTCCGCTTTGGTAAAT 2752
QY 2618 TCAGACTGCCAGATGCCAAGTACAACTCTAATCTTTGGTTTACTGTGGATCTTGTGCT 2677
Db 2753 TCTCATATCGACAGATTTTACACTATATTCGTAGCCTATGCTCCTGATGCTATCGT 2812
QY 2678 AGTAACCCGACTGTACGAAACACATGCGAAATAGGGTGATCTTTGAAAAACCTTCGGT 2737
Db 2813 CACAATCCTGATTTGGGATACGACATTAACCTATTAATGGAGCTACGTGGACCTCTATAGG 2872
QY 2738 ACGAATTTGGCAAGCAAGCTTTAGTCCTTCGTCGGAGGAACATTTTTCCTTAACTCA 2797
Db 2873 AATAATCTAACAGAAGTACTTTGCTAGTACAAAGCATCCAGCAATCCAGCAATGAT 2932
QY 2798 AATTTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGCTGGGTGCTCTGCAATACAA 2857
Db 2933 GTTCTAGAGATCTTCGGGACCTGTGGATGTGATATTCGCAGAACCTCCCGTAAATATCT 2992
QY 2858 GTAGACTTAGGAGCAAAATACCAATTTCTAATCGGT 2892
Db 2993 CTAGATATAGGAAGCAAAATTAGCAATTTTAAACCTT 3027

RESULT 4
US-09-612-402B-23
; Sequence 23, Application US/09612402B
; Patent No. 6642023
; GENERAL INFORMATION:
; APPLICANT: Jackson, W. James
; APPLICANT: Pace, John
; TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
; Patent No. 6642023
; FILE REFERENCE: 7969-086-999
; CURRENT APPLICATION NUMBER: US/09/612,402B
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/942,596
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 3354
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant Expression Vector
US-09-612-402B-23

Query Match 4.7%; Score 140.6; DB 4; Length 3354;
Best Local Similarity 48.5%; Pred. No. 6.2e-32;
Matches 549; Conservative 0; Mismatches 534; Indels 48; Gaps 4;
QY 1776 TGACTCCAGATCCTATAATGGGTGAGAAATTCATTTACGGCTATACGGGAACCTTGGGGCC 1835
Db 1970 TGACTCTAGGAATGAGATCCCTAAGTATGGCTATCAAGGAAGCTTGGCGTGG 2029
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QY 1836 CAATGTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCACTGGACTAAAACTGGCT 1895
Db 2030 ATCTTAATACAGCAAAATATGCTCCTTATATCTCTGAAAAGCTACATGGACTAAAACTGGGT 2089
QY 1896 ATATTCCTAAATCCCGAGCGTATCGGCTCTTTAGTCCCTAAATAGCTTATGGAATGCAATTTA 1955
Db 2090 ATAATCCTGGGCGTGGAGGAGTAGCTCTTTGGTTCCAAATAGTTTATGGGGATCCATTT 2149
QY 1956 TAGATATTAGCTCTCTCCATTTATTTATGGAGACTGCAAAAGGTTGCGAGGAGACC 2015
Db 2150 TAGATATACGATCTCGCATTCAGCAATTCAGCAAGTGTGATGGGGCTCTTTATTTGTC 2209
QY 2016 GTGCTTTTGGTGTGCTGATATCTAATCTTCTCCATTAAGATAGTACAAAAACAGCAC 2075
Db 2210 GAGGATATTGGGTTTCTCGAGTTTCGAATTTCTCTATCATGACCGCATGCTTTAGGTG 2269
QY 2076 GCGGGTTTCGCCATTTAGTGGCGGTATGTATAGGAGGAAACCTACATATCTGTTTCTAG 2135
Db 2270 AGGATATCGGTATATTAGTGGGGTTATCTCTTAGGAGCAAACTCTTCTTGGATCA- 2328
QY 2136 ATAAGATTCTTAGTGTGCTGCTTTGTCTAGCTCTTTTGGAGAGATAGAGACTTCTTTGTAG 2195
Db 2329 --TCGATGTTTGGTCTAGCAATTTACTGAAGTATTTGGTAGATCTAAAGATTATGTAGTGT 2386
QY 2196 CTAAGAAATCAAGGTACAGTCTACGGAGGAACCTCTCTATTTACCAGCACACGAACCTATA 2255
Db 2387 GTCTGTTCCAATCATCATGCTTGATAGGATCGGTTTATCTATCTACCAA----- 2435
QY 2256 TCTCTCTTCTTGTCAAACTACGGCCTTGTTCGTTCTTATCTTCTTCTTCTACAGAGATTCCTG 2315
Db 2436 -----ACAGGCTTTATGTGGATCTTATGTGTTGGAGATGCGTTTA 2476
QY 2316 TTCTCTTTTACGAAACCTTAGCTACACCATACGGATTAACGATCTGAAAAACAAGTATA 2375
Db 2477 TTC-----GTGCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2524
QY 2376 CAACATATCCTACTGTTAAAGAACTGGGGAATGATAGTTTCGTTTGAATTCGGGTG 2435
Db 2525 CATTTGCAGAGGAGAGCGGATGTTTGTGGGATAATACTGTCTGTTGGAGAGATGGAG 2584
QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAAGTGTCTATTTGAGCAGTACATG---CCCTTCA 2492
Db 2585 TGGGATACCGATTTGATTTACTCCATCTAAGCTCTATTTGAATGAGTTGCGTCTTTTCG 2644
QY 2493 TGAATTTGCAAGTTGTTGTTATGACATCAGGAAGGTTTAAAGAAACAGGGAACAGAGCTC 2552
Db 2645 TGCAGAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGGAAGCGGATCAAGCTC 2704
QY 2553 GTGAATTTGGAAGTAGCGCTCTTGTGAATCTTTCCTTACCTATCGGGATCCGATTTGATA 2612
Db 2705 GGGCATTTAGGAGTGACATCTCATGAATCTATCAGTTCTGTTGGAGTAAATTTGATC 2764
QY 2613 AGGAATCAGACTGCCAAGATGCAACGTAACAATCTTCTGTTTACTGTGGAATCTTGT 2672
Db 2765 GATGTTCTAGTACACACCCCTTAATAATATAGCTTTTATGGGGCTTATATCTGTGATGCTT 2824
QY 2673 TTGCTAGTAAACCCGACTGTACGAACACTCGGAATTTAGCGGTGATTTCTGGAAACCT 2732
Db 2825 ATCGCACCATCTCTGGGACTCAGAACACACTCTCTCCATCAAGAGAGATGAGCAACAG 2884
QY 2733 TCGGTACGAATTTGGCAAGACAGCTTTTAGTCTCTCGTCAGGGAACCAATTTTGTCTTA 2792
Db 2885 ATGCTCTTTCATTTGGCAAGACATGGAGTATAGAGGTTCTATGTATGTTCTCTAA 2944
QY 2793 ACTCAAAATTTTGAAGCTTTTAGCCAAATTTTCTTTTGAATTTGCGTGGGTCACTTCGCAAT 2852
Db 2945 CAAGCAATATAGAGTATATGCGCAATGGAAGATATGAGTATCGAGATCTTCTCGAGGT 3004
QY 2853 ACATGTAGACTTAGGAGCAAAATACCAATTTCTAATGCGGTAGCTTTGGTA 2903
Db 3005 ATGCTTTGAGTGCAGGAAGTAAAGTCCGGTTCTAAAAAATATTGTTTAGATA 3055
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RESULT 5
US-09-612-402B-24
; Sequence 24, Application US/09612402B
; Patent No. 6642023
; GENERAL INFORMATION:
; APPLICANT: Jackson, W. James
; APPLICANT: Pace, John
; TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
; Patent No. 6642023
; FILE REFERENCE: 7969-086-999
; CURRENT APPLICATION NUMBER: US/09/612,402B
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/942,596
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 24
; LENGTH: 3324
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant Expression Vector
US-09-612-402B-24

Query Match 4.5%; Score 133.8; DB 4; Length 3324;
Best Local Similarity 48.7%; Pred. No. 7.2e-30;
Matches 551; Conservative 0; Mismatches 532; Indels 48; Gaps 5;

QY 1776 TGACTCCAGATCCTATAATGGGTGAGAAATTCATTACGGCTATCAGGGAACCTTGGGGCC 1835
DB 1973 TGACTCTAGGGAATGAGATGCCCTAAGTATGGCTATCAAGGAAGCTGGAAGCTTGGCGGG 2032

QY 1836 CAATTGTTTGGGGCAGAGGGCTTCTACGACTGCAACCTTCACTGACTTAAACTGGCT 1895
DB 2033 ATCCCTAATACAGAAATATATGTCCTTACTCTGAAAGTACATGACTTAAACTGGGT 2092

QY 1896 ATATCTCTAATCCGAGCGTATGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTA 1955
DB 2093 ATAACTCTGGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTATGGGGATCCATTT 2152

QY 1956 TAGATATTAGCTCTCTCCATTAATCTTATGGAGACTGCAACGAAGGGTTGCGAGGAGACC 2015
DB 2153 TAGATATAGCATCTGGCATTCAGCAATTCAGCAAGTGTGGATGGCGCTCTTATGTC 2212

QY 2016 GTGCTTTTGGTGTGCTGATTAATCTAAGTCTTCCATAGGATAGTACAAAACAGAC 2075
DB 2213 GAGGATATGGGTTCTGGAGTTTCGAATTTCCCTATCATGACCGCGAGTCTTTAGGTC 2272

QY 2076 GCGGGTTTCGCCATTTGAGTGGCGGTATGTCTATAGGAGGAAACCTPACATCTTGTTCAG 2135
DB 2273 AGGGATATCGGTATATTAGTGGGGTTATTCCTTAGGAGCAAACTCTACTTTGGATCA- 2331

QY 2136 ATAAGATCTTAGTGTGATTTGTGACGTCTTTGGAGAGATAGAGACTACTTTGTAG 2195
DB 2332 --TCGATGTTTGGCTPAGCATTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTG 2389

QY 2196 CTAAGAATCAAGGTACAGTCTACGGGAACTCTCTATTACCAGCACACGAAACCTATA 2255
DB 2390 GTCGTTCCAAATCATGCTTGCATAGGATC-----CGTTA 2426

QY 2256 TCTCTCTCTCTGCAAACTACGGCCCTTTGTTGGTGTCTTATGTTCTACAGAGATTCCTG 2315
DB 2427 TCTATCTACAAACAAGCT-----TTATGTGGATCCTATTGTTCCGGAGATCGGT 2477

QY 2316 TTCTCTTTTCAGGAACCTTAGCTACACCCATACGGATACGATCTGAAACCAAGTATA 2375
DB 2478 TATCCGT-----GCTAGTACGGGTTTGGGAACCAAGATATGAAACCTCATACA 2527

QY 2376 CAACATATCTCTGTTAAAGGAAGCTGGGGAATCATAGTTTCGCTTTTGAATTCGGTG 2435
DB 2528 CATTCAGAGGAGCGGATGTTCTGTTGGGATATAAATCTGTCTGGTTGGAGATTTGGAG 2587

QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAAGTCTCTATTGAGCAGTACATG---CCCTTCA 2492

DB 2588 TGGGATTACCGATTGTGACTACTCCATCTAAGCTCTATTGAATGAGTTGCGCTCTTCG 2647
QY 2493 TGAATTTGCAAGTTTGTCTATGCACATCAGGAAGGTTTTTAAAGAACAGGAACAGAGCTC 2552
DB 2648 TGAAGCTGAGTTTTCTTATGCGGATCATGAATCTTTTACAGAGGAAGGCGATCAAGCTC 2707
QY 2553 GTGAATTTGGAAGTAGCGCTCTTGTGAATCTTGCCTTACCTATCGGATCCGATTTGATA 2612
DB 2708 GGGCATTCAGGAGTGTCTATCTCATGAATCTATCAGTTCCTGTTGGAGTAAAAATTTGATC 2767
QY 2613 AGGAATCAGACTGCCAAGATGCAACGTCACAATCTAATCTTGTGTTATCTGTGGAATCTTG 2672
DB 2768 GATGTTCTAGTACACACCCCTAATAATATAGCTTTTATGGGGCTTATATCTGTGATGCTT 2827
QY 2673 TTCTAGTAAACCCGACTGTACGACAACTGCGGAATAGCGGTGATTTCTGGAAACCT 2732
DB 2828 ATCGCACCATCTCTGGGACTCAGAACACCTCTATCCCATCAAGAGACATGGAACAACAG 2887
QY 2733 TCGGTACGAATTTGGCAAGACAGCTTTAGTCTCTTCGTCAGGGAACCAATTTTGCCTTA 2792
DB 2888 ATGCCCTTCATTTGGCAAGACATGGAGTCATAGTTAGGGTCTATGTAAGTCTTCTCTAA 2947
QY 2793 ACTCAAATTTGAAGCCTTTAGCCAAATTTCTTTTGAATTTGGTGGGTCTATCTCGCAAT 2852
DB 2948 CAAGCAATATAGAAGTATATGCCCATGGAAGATATGAGTATCGAGATCTTCTCGAGGT 3007
QY 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAATGCGTTAGCTTTGGTA 2903
DB 3008 ATGGTTTGAAGTGCAGGAAGTAAAGTCCGGTTCTTAAATAATTTGGTTAGATA 3058

RESULT 6
US-09-556-877-182
; Sequence 182, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.489C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-182

Query Match 4.4%; Score 132.2; DB 4; Length 3021;
Best Local Similarity 48.8%; Pred. No. 2.1e-29;
Matches 544; Conservative 0; Mismatches 523; Indels 48; Gaps 5;

QY 1776 TGACTCCAGATCCTATAATGGGTGAGAAATTCATTACGGCTATCAGGGAACCTTGGGGCC 1835
DB 1952 TGACTCTAGGGAATGAGATGCTTAAGTATGGCTATCAAGGAAGCTTGGGTGGG 2011
QY 1836 CAATTTGTTGGGGCAGGGGCTTCTACGCTGGAACCTTCACTGGAATAAATCTGGCT 1895
DB 2012 ATCTAATACAGCAAAATATGTTCTCTATCTCTGAAAGCTACATGGAATAAATCTGGT 2071
QY 1896 ATATCTCTAATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTA 1955
DB 2072 ATAACTCTGGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 2131
QY 1956 TAGATATTAGCTCTCTCCATTAATCTTATGAGACTGCAACGAAGGTTTGCAGGAGACC 2015

Db 2132 TAGATATACGATCTCGCATTCAGCAATTCAGCAAGTGTGGATGGCGCTCTTATTGTC 2191
Qy 2016 GTGCTTTTGTGCTGATTAATCTAATCTCTCCATAAGGATAGTACAAAACACGAC 2075
Db 2192 GAGGATTAAGGTTCTGGAGTTTGAATTTCTTATCATGACCGGATGCTTTAGTGC 2251
Qy 2076 GCGGTTTTCGCAATTTAGTGGCGGTTATGTATAGGAGGAAACCTCATACTTTGTCAG 2135
Db 2252 AGGATATCGGTATATAGTGGGTTATTCTTAGGAGCAAACTCTTACTTTGGATCA- 2310
Qy 2136 ATAGATTTCTAGTCTGATTTGTCAGTCTTTGGAGAGATAGACACTTTGTTAG 2195
Db 2311 --TCGATTTTGGTCTAGCATTTACCGAAGTATTGGTAGATCTAAGATTTATGTAGTGT 2368
Qy 2196 CTAAGATCAAGGTACAGTCTACGAGGAACTCTATTACCAGCACAAACCAACTATA 2255
Db 2369 GTGCTTCAATCATCATGCTTGCATAGATC-----CGTTTA 2405
Qy 2256 TCTCTTTCTTTCGAAACTACGGCTTGTCTGTTGTTCTTATGTTCTTCTACAGATTTCTG 2315
Db 2406 TCTATCTACCAACAAGCT-----TTATGTGATCTTATTGTTGGAGATGCGTT 2456
Qy 2316 TCTCTTTTTCAGGAAACCTTAGCTACACCCATACGATAACGATCTGAAACCAAGTATA 2375
Db 2457 TATCGGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2506
Qy 2376 CAACATATCTTACTGTTAAAGCAAGCTGGGGAATGATAGTTTCGTTTATAGAAATTCGGTG 2435
Db 2507 CATTTGAGAGAGAGCGATGTTCTGGGATATTAACGTCTGCTGGAGAGATTGGAG 2566
Qy 2436 GAAGAGCTCCGATTTGCTAGATGAAGTCTCTATTGTTGAGCAGTACATG---CCTTTCA 2492
Db 2567 CGGATTAACCGATTGTGATTAATCTCAATCAAGCTCTATTGAAATGAGTTGGTCTCTTCG 2626
Qy 2493 TGAATTCAGTTTCTATGACATCAGGAGGTTTAAAGAACAGGAAACAGAGCTC 2552
Db 2627 TCGAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGAAAGCGGATCAAGCTC 2686
Qy 2553 GTGAATTTGGAGTAGCGCTGTTGAAATCTTGGAATCTTGCCCTTACCTATCGGATTCGATTTGATA 2612
Db 2687 GGGCATTCAGAGCGGACATCTCTTAATCTATCAGTTTCTGTTGGAGTGAATTTGATC 2746
Qy 2613 AGGAATCAGATGCCAAGATGCAAGTCAATCTAATCTTGGTTATGTTGATGTTGATCTG 2672
Db 2747 GATGTTCTAGTACACATCTTAATAAATATAGCTTTATGCGGCTTATATCTGTGATGCTT 2806
Qy 2673 TCGTAGTAAACCCGACTGTAGCAACACCTCGAATTAGCGGTGATTTCTTGGAAACCT 2732
Db 2807 ATCGCACCATCTCTGGTACTGAGACACGCTCTTATCCCATCAAGAGACATGGACAACAG 2866
Qy 2733 TCGGTACGAATTTGGCAAGACAGCTTTTAGTCTTTCGTGCGAGGAAACCATTTTTCCTTTA 2792
Db 2867 ATGCTCTTCAATTTAGCAAGACATGAGTTGTTGTTAGAGATCTATGATGCTTCTCTAA 2926
Qy 2793 ACTCAATTTTGAAGCTTTAGCCAAATTTCTTTGAAATGGTGGGTCACTCCCAATT 2852
Db 2927 CAAGTAATATAGAGTATATGCGCCATGGAAGATATGAGTATCGAGATGCTTCTCGAGCT 2986
Qy 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAA 2887
Db 2987 ATGTTTGAGTGCAGGAAGTAAAGTCCCGTTCTAA 3021

RESULT 7

US-09-620-412C-182

; Sequence 182, Application US/09620412C

; Patent No. 6448234

; GENERAL INFORMATION:

; APPLICANT: Steven P. Fling

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

; FILE REFERENCE: 210121.469C7

; CURRENT APPLICATION NUMBER: US/09/620,412C

; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-182

Query Match 4.4%; Score 132.2; DB 4; Length 3021;
Best Local Similarity 48.8%; Pred. No. 2.1e-29;
Matches 544; Conservative 0; Mismatches 523; Indels 48; Gaps 5;
Qy 1776 TGAATCCAGATCCCTATATATGGGTGAGAAATTCCTATACGGCTATCAGGAACTTTGGGGCC 1835
Db 1952 TGAATCCAGGATGAGATGCTTAAGTATGCTATCAAGGAAGCTTGAAGCTTTGGTGGG 2011
Qy 1836 CAATGTTTGGGACAGGGGCTTCTACGACTGCAACCTTCACTGGACTAAACTGGCT 1895
Db 2012 ATCTAATACAGCAAAATATGCTCTTATATCTGAAAGCTACATGGACTAAACTGGGT 2071
Qy 1896 ATATTCTAATCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTTA 1955
Db 2072 ATATCTGGGCTGAGGAGTAGTCTTTTGGTTCCAAATAGTTTATGGGATCCATTT 2131
Qy 1956 TAGATATTAGTCTCTCCATTTATCTTATGGAGACTGCAACGAAAGGTTGAGGGAGACC 2015
Db 2132 TAGATATACGATCTCGCATTCAGCAATTCAGCAAGTGTGATGGGCGCTCTTATTGTC 2191
Qy 2016 GTGCTTTTGGTGTGCTGATTAATCTAATCTTCTCCATAAGGATAGTACAAAACACGAC 2075
Db 2192 GAGGATTAAGGTTTCTGGAGTTTCGAATTTCTTCTATCATGACCGGATGCTTTAGTGC 2251
Qy 2076 GCGGTTTTCGCAATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTCATACTTTGTTGAG 2135
Db 2252 AGGATATCGGTATATAGTGGGTTTATCTCTTAGGAGCAAACTCTTACTTTGGATCA- 2310
Qy 2136 ATAGATTTCTAGTCTGCTCAATTTGTGCTGCTTTTGAAGAGATAGAGACTTCTTTGTTAG 2195
Db 2311 --TCGATTTTGGTCTAGCAATTTACCGAAGTATTGGTAGATCTAAGATTTATGTAGTGT 2368
Qy 2196 CTAAGATCAAGGTACAGTCTACGAGGAACTCTCTATTACCAGCACAAACCAACTATA 2255
Db 2369 GTGCTTCAATCATCATGCTTGCATAGATC-----CGTTTA 2405
Qy 2256 TCTCTTCTCTTGCAAACTACGGCTTGTGTTGTTCTTATGTTCTTCTACAGAGATTCCTG 2315
Db 2406 TCTATCTACCAACAAGCT-----TTATGTGATCTTATTGTTGGAGATGCGTT 2456
Qy 2316 TCTCTTTTTCAGGAAACCTTAGCTACACCCATACGGAATACGATCTGAAACCAAGTATA 2375
Db 2457 TATCGGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2506
Qy 2376 CAACATATCTTACTGTTAAAGCAAGCTGGGGAATGATAGTTTCGTTTATAGAAATTCGGTG 2435
Db 2507 CATTTGAGAGAGAGCGATGTTCTGGGATATTAACGTCTGCTGGAGAGATTGGAG 2566
Qy 2436 GAAGAGCTCCGATTTGCTAGATGAAGTCTCTATTGTTGAGCAGTACATG---CCTTTCA 2492
Db 2567 CGGATTAACCGATTGTGATTAATCTCAATCAAGCTCTATTGAAATGAGTTGGTCTCTTCG 2626
Qy 2493 TGAATTCAGTTTGTCTATGCAATCAGGAGGTTTAAAGAACAGGAAACAGAGCTC 2552
Db 2627 TCGAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGAAAGCGGATCAAGCTC 2686
Qy 2553 GTGAATTTGGAGTAGCGCTGTTGAAATCTTGGAATCTTGCCCTTACCTATCGGATTCGATTTGATA 2612
Db 2687 GGGCATTCAGAGCGGACATCTCTTAATCTATCAGTTTCTGTTGGAGTGAATTTGATC 2746
Qy 2613 AGGAATCAGATGCCAAGATGCAAGTCAATCTAATCTTGGTTATGTTGATGTTGATCTG 2672
Db 2747 GATGTTCTAGTACACATCTTAATAAATATAGCTTTATGCGGCTTATATCTGTGATGCTT 2806
Qy 2673 TCGTAGTAAACCCGACTGTAGCAACACCTCGAATTAGCGGTGATTTCTTGGAAACCT 2732
Db 2807 ATCGCACCATCTCTGGTACTGAGACACGCTCTTATCCCATCAAGAGACATGGACAACAG 2866
Qy 2733 TCGGTACGAATTTGGCAAGACAGCTTTTAGTCTTTCGTGCGAGGAAACCATTTTTCCTTTA 2792
Db 2867 ATGCTCTTCAATTTAGCAAGACATGAGTTGTTGTTAGAGATCTATGATGCTTCTCTAA 2926
Qy 2793 ACTCAATTTTGAAGCTTTAGCCAAATTTCTTTGAAATGGTGGGTCACTCCCAATT 2852
Db 2927 CAAGTAATATAGAGTATATGCGCCATGGAAGATATGAGTATCGAGATGCTTCTCGAGCT 2986
Qy 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAA 2887
Db 2987 ATGTTTGAGTGCAGGAAGTAAAGTCCCGTTCTAA 3021


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Query Match 4.4%; Score 132.2; DB 4; Length 4435;
Best Local Similarity 48.6%; Pred. No. 2.7e-29;
Matches 550; Conservative 0; Mismatches 533; Indels 48; Gaps 5;

QY 1776 TGACTCCAGATCCCTATATAGTGGTGAAGAAATCCCAATACCGCTATCAGGCTATCAGGAACTTGGGGCC 1835
DB 2351 TGACTCTAGGGAATGAGATGCTTAAGTATGCTATCAAGGAAGCTTGGAGCTTGGCTGGG 2410

QY 1836 CAATTTGTTGGGGACAGGGCTTCTACGCTGCAACCTTCAACTGGACTAAACCTGGCT 1895
DB 2411 ATCTTAATACAGCAATTAATGCTTCTATATCTGAAGCTACATGGACTAAACTGGGT 2470

QY 1896 ATATTCCTTAATCCCGAGCGTATCGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTA 1955
DB 2471 ATAACTCTGGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 2530

QY 1956 TAGATATTAGCTCTCTCCATTTCTTATGGAGACTGCAACGAAGGTTGAGGGAGACC 2015
DB 2531 TAGATATACGATCTGCGCAATTCAGCAATTCAGCAAGTGTGGATGGGCGCTCTTATGTC 2590

QY 2016 GTGCTTTTGGTGTGCTGGATTTCTAACTTCTTCCATAAGGATAGTACAAAAACAGCAC 2075
DB 2591 GAGGATTAATGGTTCTGAGGTTTCGATTTCTTCTATCATGACCGCATGCTTTAGTGC 2650

QY 2076 GCGGTTTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATCTTTGTCAG 2135
DB 2651 AGGGATATCGGTATATTAGTGGGGTTATCTCTAGGAGCAACTCTCTACTTTGGATCA- 2709

QY 2136 ATAGATTTCTTAGTCTGCTCAATTTGTGCTCTTTGGAAGAGATAGACTACTTTGTAG 2195
DB 2710 --TCGATGTTTGGTCTAGCATTTACCGAAGTATTTGGTAGATCTTAAGATTTATGTAGTGT 2767

QY 2196 CTAAGAAATCAAGGTACAGTCTACGGAGGAATCTCTATTACAGCACAAACCAACTATA 2255
DB 2768 GTGCTTCAATCATCATCTGTCATAGATC-----CGTTA 2804

QY 2256 TCTCTCTTCTTGGAAATACAGGCTTGTGCTGCTTGTATGTTCTTCTACAGATTCCTG 2315
DB 2805 TCTATCTACCAACAAAGCT-----TTATGTGGATCTTATTTGTTGGGAGATGCGTT 2855

QY 2316 TTCTCTTTTTCAGGAACCTTAGCTACACCCATACGATACGATACGATGAAACCAAGTATA 2375
DB 2856 TATCCGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2905

QY 2376 CAACATATCTACTCTTTAAAGGAACCTGGGGAATGATAGTTTTCGCTTTAGAAATTCGGTG 2435
DB 2906 CATTTGCAGAGGAGAGCGATGTTCTGTTGGATAATACTGTCTGCTGGAGAGATTGGAG 2965

QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAGTGTCTTATTTGAGCAGTACATG---CCCTTCA 2492
DB 2966 CGGGATTAACCGATTGTGATTAATCTCAAGCTCTAATGAACTGAGTTGGTTCCTTTTCG 3025

QY 2493 TGAATTCAGTTTGTCTATGCATACATCAGGAGGTTTAAAGAACAGGAAACAGAGCTC 2552
DB 3026 TGCAGCTGAGTTTCTTATGCGGATCATGATCTTTTACAGAGGAGCGCATCAAGCTC 3085

QY 2553 GTGAATTTGAAGTAGCGCTCTTGTGAATCTTGTCCCTTACCTATCGGGATCCGATTTGATA 2612
DB 3086 GGGCAATCAAGAGCGGACATCTCTTAATCATCATAGTTCCCTGTTGAGTGAGTTTGATC 3145

QY 2613 AGGAATCAGCTGCCAAGATGCAACGATCAATCTAACTCTTGGTTTATCTGTGGATCTTG 2672
DB 3146 GATGTTCTAGTACACATCTTAATAAATATAGCTTTATGGCGGCTTATATCTGTGATGCTT 3205

QY 2673 TTGCTAGTAAACCCGACTGTACGACACACTGCGAATTAGCGGTGATTTCTTGGAAACCT 2732
DB 3206 ATCGACACCATCTCTGCTACTGAGACAAACGCTCTTATCCATCAAGAGACATGGACACAG 3265

QY 2733 TCGGTACGAATTTGGCAAGACGCTTTAGTCTTCTTGTGCGAGGGAACCAATTTTGCCTTA 2792
DB 3266 ATGCTCTTCAATTTAGCAAGACATGAGTTGTGGTTAGAGGATCTATGTATGCTTCTCTAA 3325

QY 2793 ACTCAAAATTTGAAGCCTTTACCCAAATTTCTTTTGAATTTGGTGGGTCACTCGCAATT 2852

Db 3326 CAAGTAATATAAGATATATGCGCATGAGATATAGTATCGAGATCTTCTCGAGGCT 3385
QY 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTTAATGCTTGTAGCTTTGGTA 2903
Db 3386 ATGGTTTGTAGTGCAGGAAGTAGATCCGGTTCTTAAATAATTTGTTAGATA 3436

RESULT 10
US-09-556-877-170
; Sequence 170, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556.877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-170

Query Match 4.4%; Score 131.4; DB 4; Length 2949;
Best Local Similarity 48.6%; Pred. No. 3.6e-29;
Matches 542; Conservative 2; Mismatches 523; Indels 48; Gaps 5;

QY 1776 TGACTCCAGATCCCTATATAGTGGTGAAGAAATTCCTATACGGCTATCAGGAACTTGGGGCC 1835
DB 1880 TGACTCTAGGGAATGAGATGCTTAAGTATGCTATCAAGGAAGCTTGGAGCTTGGCTGGG 1939

QY 1836 CAATTTGTTGGGGACAGGGCTTCTACGCTGCAACCTTCAACTGGACTAAACCTGGCT 1895
DB 1940 ATCTTAATACAGCAATTAATGCTTCTTATATCTCTGAAGCTACATGGACTAAACCTGGT 1999

QY 1896 ATATTCCTTAATCCCGAGCGTATCGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTA 1955
DB 2000 ATAACTCTGGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 2059

QY 1956 TAGATATTAGCTCTCTCCATTTCTTATGGAGACTGCAACGAAGGTTGAGGGAGACC 2015
DB 2060 TAGATATACGATCTGCGCAATTCAGCAATTCAGCAAGTGTGGATGGGCGCTCTTATGTC 2119

QY 2016 GTGCTTTTGGTGTGCTGGATTTCTAACTTCTTCCATAAGGATAGTACAAAAACAGCAC 2075
DB 2120 GAGGATTAATGGTTCTGAGGTTTCGATTTCTTCTATCATGACCGCATGCTTTAGTGC 2179

QY 2076 GCGGTTTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATCTTTGTCAG 2135
DB 2180 AGGGATATCGGTATATTAGTGGGGTTATCTCTTAGGAGCAACTCTCTACTTTGGATCA- 2238

QY 2136 ATAGATTTCTTAGTCTGCTCAATTTGTGCTGCTTTTGGGAAGAGATAGACTACTTTGTAG 2195
DB 2239 --TCGATGTTTGGTCTAGCATTTACCGAAGTATTTGGTAGATCTTAAGATTTATGTAGTGT 2296

QY 2196 CTAAGAAATCAAGGTACAGTCTACGGAGGAATCTCTATTACAGCACAAACCAACTATA 2255
DB 2297 GTGCTTCCATCATCATCTGCTTGCATAGATC-----CGTTA 2333

QY 2256 TCTCTCTTCTTGGAACTAGCGCTTGTGCTGCTTCTTATGTTCTTCTACAGATTTCTG 2315
DB 2334 TCTATCTACCAACAAAGCT-----TTATGTGGATCTTATTTGTTGGGAGATGCGGT 2384

QY 2316 TTCTCTTTTTCAGGAACCTTAGCTACACCCATACGGAATACGATCTGAAACCAAGTATA 2375
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Db 2385 TATCCGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2434
QY 2376 CAACATATCTACTGTGTTAAAGGAAGCTGGGGGATGATAGTCTTCGCTTTAGAAATTCGGTG 2435
Db 2435 CATTCGAGGAGAGAGGATGTCGTTGGGATATTAACCTCTCGCTGGGAGATTTGGAG 2494
QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAGTCTCTATTTGAGCAGTACATG---CCCTTCA 2492
Db 2495 CGGGATTACCGATTGATTAATCTTAAGCTCTAATTTGAATGAGTTGCGTCTTTCG 2554
QY 2493 TGAATTTGCAATTTGCTATGCAATCAGCAAGAGGTTTAAAGAACAGGAAACAGAGCTC 2552
Db 2555 TCGAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGGAAGCGATCAAGCTC 2614
QY 2553 GTCAATTTGGAAGTACCGCTTGTGTAATCTTCGCTTACCTATCGGATCCGATTTGATA 2612
Db 2615 GGGCAITTAAGAGCGGACATCTCTAATCTATCAGTTCTCTGTGAGTGAAGTTTGATC 2674
QY 2613 AGGAATCAGACTGCCAAGATGCAACGTACAATCTAATCTTGTGTTTATCTGTGATCTTG 2672
Db 2675 GATGTTCTAGTACACATCTTAATAATATAGCTTTATGGCGCTTATCTGTGATGCTT 2734
QY 2673 TTCGTAAGTACCCGACTGTACGACAACTCGAATTAGCGGTGATTTCTGGAAACCT 2732
Db 2735 ATCGACCATCTCTGTACTGAGCAACGCTCTATCCCATCAAGAGACATGGAACAACAG 2794
QY 2733 TCGGTACGAATTTGGCAAGAACGTTTACTCTCTCGTGCAGGGAACCAATTTTGTCTTA 2792
Db 2795 ATGCTTTCAATTTAGCAAGACATGAGTTGTGTTAGAGATCTATGATGCTTCTCTAA 2854
QY 2793 ACTCAAAATTTGAGCGCTTTAGCCAAATTTCTTTTGAATTCGTTGGGTCACTCGCAAT 2852
Db 2855 CAAGTAATATAGAAGTATATGSCCATGGAAGATAGATCCAGATGCTTCTCGAGGCT 2914
QY 2853 ACATGTAAGCTTAGAGCAAAATACCAATCTAA 2887
Db 2915 ATGGTTTGAAGTCAGGAGMAGTAAGTCYGGTTCTAA 2949

RESULT 11
US-09-620-412C-170
; Sequence 170, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-170

Query Match 4.4%; Score 131.4; DB 4; Length 2949;
Best Local Similarity 48.6%; Pred. No. 3.6e-29;
Matches 542; Conservative 2; Mismatches 523; Indels 48; Gaps 5;
QY 1776 TGAATCCAGATCCTATAATGGGTGAGAAATTCATTACGCTATACGGAACCTTGGGCGC 1835
Db 1880 TGAATCCAGATGAGATGCTTAAGTATGGCTATCAAGAGCTGGAAGCTTGGCTGGG 1939
QY 1836 CAATTTGTTGGGAGCAGGGGCTTCTACGACTGCAACCTTCAACTGGACTTAAACCTGGCT 1895
Db 1940 ATCCTAATACAGCAATAATGGTCTTATACCTGTAAGCTACATGCACTAAACCTGGCT 1999
QY 1896 ATATTCCTAATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTA 1955
Db 2000 ATAATCCTGGGCTGAGCGAGTAGCTTCTTTGTTGCAAAATAGTTTATGGGATCCATTT 2059

QY 1956 TAGATATTAGCTCTCTCCATTATCTTATGAGACTGCAACAGAGGGTTTCAGGGAGACC 2015
Db 2060 TAGATATAGATCTGGCATTTAGCAATTCAGCAAGTGTGGATGGGCGCTCTTATTGTCT 2119
QY 2016 GTCTTTTTGGTGTCTGGATTTATCTAACTCTTCCATAGGATAGTACAAAACACGAC 2075
Db 2120 GAGGATTATGGGTTCTGGAGTTTCGAATTTCTTCTATCATGACCGGATGCTTTAGTCT 2179
QY 2076 GCGGGTTTCGCCAATTTGAGTGGCGGTTATGTCTATAGGAGAAACCTTACATCTTGTTCAG 2135
Db 2180 AGGGATATCGGTATATTAGTGGGGTTTATCTCTTAGGAGCAAACTCTACTTTTGGATCA- 2238
QY 2136 ATPAAGATTTCTAGTGTCTGATTTTCTCAGCTCTTTTGGAGAGATAGAGACTACTTTGTAG 2195
Db 2239 --TCGATGTTGGTCTAGCATTTTACCGAAGTATTTGGTAGATCTAAGATTTATGTAGTGT 2296
QY 2196 CTAAAGATCAAGGTACAGTCTACGAGGAACCTCTCTATTACCAGCACAAACCAACCTATA 2255
Db 2297 GTCGTTCCAATCATCATGCTTGCATAGGATC-----CGTTTA 2333
QY 2256 TCTCTCTTCTTCTGCAAACTACGGCCTTGTGTTGTTGTTCTTATGTTCTTACAGATTTCTCTG 2315
Db 2334 TCTATCTACCCCAACAAGCT-----TTATGTGATCTCTATTTGTTTCGGAGATGCGTT 2384
QY 2316 TTTCTCTTTTTCAGGAACCTTAGCTACACCATACGATACGATCTGAAACCAAGTATA 2375
Db 2385 TATCCGT-----GCTAGCTCGGGTTTGGGAATCAGCATATGAAACCTCATATA 2434
QY 2376 CAACATATCTACTGTGTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAAATTCGGTG 2435
Db 2435 CATTTGCAGAGGAGAGCGATGTTGTTGGATTAATACTGTCTGGCTGGAGATTTGGAG 2494
QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAGTGTCTCTATTGAGCAGTACATG---CCCTTCA 2492
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Db 2555 TCGAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGGAAGCGATCAAGCTC 2614
QY 2553 GTGAATTTGGAAGTAGCCGCTTGTGTAATCTTTCGCTTACCTATCGGGAATCCGATTTGATA 2612
Db 2615 GGGCAITTAAGAGCGGACATCTCTAATCTATCAGTCTCTGTTGGAGTCAAGTTTGTATC 2674
QY 2613 AGGAATCAGACTGCCAAGATGCAACGTAACAATCTACTCTTGTGTTATATCTGTGAGTCTTG 2672
Db 2675 GATGTTCTAGTACACATCTCTAATAATAATATAGCTTTATGGCGCTTATATCTGTGATGCTT 2734
QY 2673 TTCGTAAGTACCCGACTGTACGACAACTCGAATTAGCGGTGATTTCTGGAAACCT 2732
Db 2735 ATCGACCATCTCTGTACTGAGCAACGCTCTATCCCATCAAGAGACATGGAACAACAG 2794
QY 2733 TCGGTACGAATTTGGCAAGCAAGCTTTTAGTCTCTGTCAGGGAACCAATTTTGTCTTA 2792
Db 2795 ATGCTTTTCAATTTAGCAAGCATGAGTTGTGTTAGAGATCTATGATGCTTCTCTAA 2854
QY 2793 ACTCAAAATTTGAGCGCTTTAGCCAAATTTCTTTTGAATTTGCGTGGGTGATCTCGCAAT 2852
Db 2855 CAAGTAATATAGAAGTATATGSCCATGGAAGATAGATCCAGATGCTTCTCGAGGCT 2914
QY 2853 ACATGTAAGCTTAGAGCAAAATACCAATCTAA 2887
Db 2915 ATGGTTTGAAGTCAGGAGMAGTAAGTCYGGTTCTAA 2949

RESULT 12
US-09-598-419-170
; Sequence 170, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John

;; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
;; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
;; FILE REFERENCE: 210121.459C6
;; CURRENT APPLICATION NUMBER: US/09/598,419
;; CURRENT FILING DATE: 2000-06-20
;; NUMBER OF SEQ ID NOS: 357
;; SOFTWARE: FastSeq for Windows Version 3.0/4.0
;; SEQ ID NO 170
;; LENGTH: 2949
;; TYPE: DNA
;; ORGANISM: Chlamydia
US-09-598-419-170

Query Match 4.4%; Score 131.4; DB 4; Length 2949;
Best Local Similarity 48.6%; Pred. No. 3.6e-29;
Matches 542; Conservative 2; Mismatches 523; Indels 48; Gaps 5;
QY 1776 TGACTCCAGATCCCTAATATGGTGGAGAAATCCATTACGGCTATCAGGAACTGGGGCC 1835
DB 1880 TGACTCTAGGGAATGAGATGCTTAAATGCTTATCAAGGAAGCTTGAAGCTTGGCTGG 1939
QY 1836 CAATGTTTGGGGACAGGGCTTCAAGCTGCAACCTTCAACTGGACTAAACTGGCT 1895
DB 1940 ATCTTAATACAGCAATTAATGCTTCTTATCTCTGAAAGCTACATGGACTAAACTGGT 1999
QY 1896 ATATTCCTAATCCCGAGGCTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTA 1955
DB 2000 ATATCTCTGGGCTGAGCGAGTAGCTCTTTGGTTCCAAATAGTTTATGGGATCAATTT 2059
QY 1956 TAGATATAGCTCTCTCCATATCTTATGAGAGCTGCAAAAGGAGTTGCGGAGACC 2015
DB 2060 TAGATATAGCTCTCGCATTCAGCAATTCAGCAAGTGTGATGGGGCTCTTATTGTC 2119
QY 2016 GTGCTTTTGGTGTCTGCTGATATCTAATCTCTCCATAAGATAGTACAAAACAGCAC 2075
DB 2120 GAGGATTAGGTTTCTGGAGTTTCGAATTTCTTATCATGACCGAGTCTTATAGTTC 2179
QY 2076 GCGGTTTCGCCATTTGAGTGGCGGTTATGTCATAGAGGAACCTCATACATCTTCTTCAG 2135
DB 2180 AGGATATCGGTATATAGTGGGGTTATCTCTAGGAGCAACTCTCTTGTGATCA- 2238
QY 2136 ATAGATTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2195
DB 2239 --TCGATGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2296
QY 2196 CTAAGAACTCAAGGTACAGTCTACGAGGAACCTCTATTACAGCACACGAACCTATA 2255
DB 2297 GTCGTTCCATCATGCTTGCATAGATC-----CGTTA 2333
QY 2256 TCTCTCTCTCTGCAAACTACGGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2315
DB 2334 TCTATCTACCAACAAGCT-----TTATGTGATCTCTATTTGTTGCGAGATGCGTT 2384
QY 2316 TTCTCTTTTCAGAAACCTTAGCTACACCCATACGATTAACGATCTGAAACCAAGTATA 2375
DB 2385 TATCCGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2434
QY 2376 CAACATATCTACTGTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAAATCGGTG 2435
DB 2435 CATTTGACAGAGAGAGCGATGTTGTTGGGATATAAATCTGCTGCTGAGAGATGGAG 2494
QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAGTCTCTATTGAGCAGTACATG---CCCTTCA 2492
DB 2495 CGGGATTACCGATTGATTAATCTCCATCTAAGCTCTATTGAATGAGTTGCGTCTCTTGG 2554
QY 2493 TGAATTTGAGTTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2552
DB 2555 TCGAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACGAGGAAGCGGATCAAGCTC 2614
QY 2553 GTGAATTTGGAAGTACCGCTGCTGTAATCTTGGCTTACCTATCGGAGTCCGATTTGATA 2612
DB 2615 GGGCATTCAGAGCGGACATCTCTTAATCTATCAGTTCTCTGTTGGAGTTGATC 2674

QY 2613 AGGAATCAGACTGCCAAGATGCAACGTTACAACTTAACCTTCTGTTTATTAATGTTGATCTTG 2672
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QY 2793 ACTCAATTTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGGTGGTCACTCCCAAT 2852
DB 2855 CAAGTAAATATAGAATATATGCCATGGAAGATATAGTATCGAGATGCTTCTCGAGCT 2914
QY 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAA 2887
DB 2915 ATGTTTGTAGTGCAGGAGTAAAGTCYGGTTCTAA 2949
RESULT 13
US-09-612-402B-11
; Sequence 11, Application US/09612402B
; Patent No. 6642023
; GENERAL INFORMATION:
; APPLICANT: Jackson, W. James
; APPLICANT: Pace, John
; TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
; Patent No. 6642023
; FILE REFERENCE: 7969-086-999
; CURRENT APPLICATION NUMBER: US/09/612,402B
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/942,596
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Chlamydia sp.
US-09-612-402B-11

Query Match 4.4%; Score 130.6; DB 4; Length 1444;
Best Local Similarity 48.7%; Pred. No. 3.9e-29;
Matches 543; Conservative 0; Mismatches 524; Indels 48; Gaps 5;
QY 1776 TCAGTCCAGATCCCTAATATGGTGGAGAAATCCATTACGGCTATCAGGAACTTGGGGCC 1835
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QY 1836 CAATTTGTTTGGGGACAGGGCTTCTAGGACTGCAACCTTCACTGGACTAAACTGGCT 1895
DB 435 ATCTTAATACAGCAATTAATGCTCTTATCTCTGAAAGCTACATGGACTAAACTGGCT 494
QY 1896 ATATTCCTAATCCCGAGGCTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGATTTA 1955
DB 495 ATATCTCTGGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 554
QY 1956 TAGATATAGCTCTCTCCATTTATCTTATGAGACTGCAACGAGGTTTGCAGGGAGACC 2015
DB 555 TAGATATAGCTCTCGGATTCAGCAATTCAGGAAGTGTGGATGGGCGCTCTTATTGTC 614
QY 2016 GTGCTTTTGGTGTCTGATTTATCTAATCTCTTCCATAAGGATAGTACAAAAACAGAC 2075
DB 615 GAGGATTAAGGTTTCTGGAGTTTCGAATTTCTTCTATCATGACCGGATGCTTTAGTTC 674
QY 2076 GCGGTTTTCGCAATTTAGTGGCGGTTATGTCATAGGAGGAACCTACATCTTCTTCTAG 2135
DB 675 AGGGATATCGGTATATTTAGTGGGGTTATTCCTTAGGAGCAAACTCTCTACTTTGGATCA- 733
QY 2136 ATAAAGATTTAGTGTGCTGATTTGTGCTCTCTTTGGAAGAGATAGAGACTACTTTGTAG 2195

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Db 734 --TCGATGTTTGGTCTAGCAATTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGT 791
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Db 792 GTCGTTTCAATCATGCTTGCATAGATC-----CGTTTA 828
QY 2256 TCTCTCTTCTTGGAACTACGGCTTGTTCGTTGTCTTATGTTCCTTACAGAGATTCTCTG 2315
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QY 2316 TTCTCTTTTTCAGGAACTTCTAGCTACACCCATACGATTAACGATCTGAAACCAAGTATA 2375
Db 880 TATCCGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 929
QY 2376 CAACATATCTACTGTTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTTAGAATTCGGTG 2435
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QY 2853 ACATGTAGACTTAGGAGCAAAATACCAATCTTAA 2887
Db 1410 ATGTTTGTAGTGCAGGAAGTAGAGTCCGGTTCTAA 1444
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RESULT 14

US-09-427-533B-1

; Sequence 1, Application US/09427533B

; Patent No. 6649370

; GENERAL INFORMATION:

; APPLICANT: Mordin, Andrew D.

; APPLICANT: Oomen, Raymond P.

; APPLICANT: Dunn, Pamela L.

; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND

; FILE REFERENCE: 19721-009

; CURRENT FILING DATE: 1999-10-26

; PRIOR APPLICATION NUMBER: US/09/427,533B

; PRIOR FILING DATE: 1999-10-26

; PRIOR APPLICATION NUMBER: 60/106,046

; PRIOR FILING DATE: 1998-10-28

; PRIOR APPLICATION NUMBER: 60/132,271

; PRIOR FILING DATE: 1999-05-03

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 1

; LENGTH: 3050

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (101)..(2893)

US-09-427-533B-1

Query Match

Best Local Similarity 50.3%; Score 61.2; DB 4; Length 3050;

Matches 181; Conservative 0; Mismatches 173; Indels 6; Gaps 1;

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Db 2667 ACGTCTTTGATATATCGTAAAGGACCTGTCTCTTTGATTACACTCAAGGATGCTGCTT 2726

QY 2718 ATTCTTGGAAACCTTCGGTACGNAATTTGGCAAGACAGCTTTAGTCTCTTCTGCAGGGA 2777

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QY 2778 ACAATTTTGTCTTAATCAAAATTTTGAAGCCTTTAGCCAAATTTCTTTTGAATTTGGGTG 2837

Db 2787 ATATACCGAATGGAATTCATATTAAGTAGTATTTAGCGTTTAATATGATGGAGAG 2846

RESULT 15

US-09-556-877-169

; Sequence 169, Application US/09556877

; Patent No. 6432916

; GENERAL INFORMATION:

; APPLICANT: Probst, Peter

; APPLICANT: Bhatia, Ajay

; APPLICANT: Skeiky, Yasir

; APPLICANT: Fling, Steve

; APPLICANT: Maisonneuve, Jeff

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

; FILE REFERENCE: 210121.469C5

; CURRENT APPLICATION NUMBER: US/09/556,877

; NUMBER OF SEQ ID NOS: 305

; SOFTWARE: FastSeq for Windows Version 3.0/4.0

; SEQ ID NO 169

; LENGTH: 2643

; TYPE: DNA

; ORGANISM: Chlamydia

US-09-556-877-169

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Best Local Similarity 50.6%; Score 50.6; DB 4; Length 2643;

Matches 122; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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Db 1278 CGGACGCTTGTATTTTAAAGATCGCGTCTTTCGCGCCCTTCTCTCTCTCAGGATCC 1337

QY 1507 AGATTCCTGCTCGAAATGGAACGTAGGAATCTACTAGAACCTGCTGATAGTACCAT 1566

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Qy 1567 AAACAATTGGTCATTAAATCAGTTCTATAGACGGTGCAGGCAAGGCAAAAATAGAAAC 1626
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Db 1458 C 1458

Search completed: August 16, 2004, 18:46:29
Job time : 171 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 18:43:38 ; Search time 906 Seconds
(without alignments)
16247.045 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 3000

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Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303934 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2241	74.7	2241	16	US-10-312-273-20
4	546.6	18.2	2781	10	US-09-738-269-56
5	546.6	18.2	2781	14	US-10-023-437-56
6	527	17.6	2787	16	US-10-312-273-96
7	523	17.4	534	16	US-10-312-273-18
8	516.6	17.2	2787	13	US-10-312-273-34
9	514	17.1	2793	13	US-10-282-122A-18496
10	514	17.1	2793	16	US-10-312-273-46
11	509.8	17.0	1230025	16	US-10-289-762-1
12	506.6	16.9	3050	9	US-09-452-380-1
13	506.6	16.9	3050	15	US-10-324-129-1
14	503.6	16.8	2811	13	US-10-282-122A-18495

15	503.6	16.8	2811	16	US-10-312-273-154	Sequence 154, Appl
16	477	15.9	2808	9	US-09-452-380-2	Sequence 2, Appli
17	477	15.9	2808	15	US-10-324-129-2	Sequence 2, Appli
18	465.8	15.5	2787	13	US-10-282-122A-18497	Sequence 18497, A
19	465.8	15.5	2787	16	US-10-312-273-116	Sequence 116, Appl
20	348.4	11.6	2520	10	US-09-738-269-22	Sequence 22, Appl
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22	345	11.5	2526	13	US-10-282-122A-18493	Sequence 18493, A
23	345	11.5	2526	16	US-10-312-273-140	Sequence 140, Appl
24	289	9.6	1065	16	US-10-312-273-16	Sequence 16, Appl
25	284	9.5	1188	16	US-10-312-273-22	Sequence 22, Appl
26	271.8	9.1	2950	9	US-09-886-468-6	Sequence 6, Appli
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28	270.6	9.0	2769	16	US-10-312-273-42	Sequence 42, Appl
29	243.4	8.1	3150	17	US-10-352-618-1	Sequence 1, Appli
30	243.2	8.1	2922	16	US-10-312-273-4	Sequence 4, Appli
31	218	7.3	4224	9	US-09-841-132-486	Sequence 486, App
32	218	7.3	4224	13	US-10-282-122A-18494	Sequence 18494, A
33	218	7.3	4224	16	US-10-312-273-32	Sequence 32, Appl
34	148.2	4.9	487	10	US-09-738-269-54	Sequence 54, Appl
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36	140.6	4.7	3354	13	US-10-701-844-23	Sequence 23, Appl
37	140.6	4.7	3354	17	US-10-766-711-23	Sequence 23, Appl
38	135.4	4.5	3042	17	US-10-467-534-10	Sequence 10, Appl
39	133.8	4.5	3324	13	US-10-701-844-24	Sequence 24, Appl
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41	132.2	4.4	3021	9	US-09-841-132-182	Sequence 182, App
42	132.2	4.4	4435	13	US-10-701-844-1	Sequence 1, Appli
43	132.2	4.4	4435	17	US-10-766-711-1	Sequence 1, Appli
44	131.4	4.4	2949	9	US-09-841-132-170	Sequence 170, App
45	130.6	4.4	1444	13	US-10-701-844-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

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US-09-428-122-1
; Sequence 1, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Murdin et al.
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 19721-007-019
; CURRENT APPLICATION NUMBER: US/09/428,122
; CURRENT FILING DATE: 1999-10-27
; EARLIER APPLICATION NUMBER: 60/106,046
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/132,271
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)...(2884)
US-09-428-122-1

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Query Match 100.0%; Score 3000; DB 10; Length 3000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1801 GAAATTCCTATTCAGGCTATCAGGGAACCTTGGGGCCCAATTTGTTGGGGGACAGGGGCTTC 1860
Db 33457 GAAATTCCTATTCAGGCTATCAGGGAACCTTGGGGCCCAATTTGTTGGGGGACAGGGGCTTC 33516
QY 1861 TAGACTGCAACCTTCAACTGGAACCTAAACTGGCTATATTCCTAAATCCCGAGGCTATCGG 1920
Db 33517 TAGACTGCAACCTTCAACTGGAACCTAAACTGGCTATATTCCTAAATCCCGAGGCTATCGG 33576
QY 1921 CTCTTTAGTCCCTTAATAGCTTTATGGAATGCAATTTATAGATATTAGCTCTCTCCATTTATCT 1980
Db 33577 CTCTTTAGTCCCTTAATAGCTTTATGGAATGCAATTTATAGATATTAGCTCTCTCCATTTATCT 33636
QY 1981 TATGAGACTGCAAAACGAAGGGTTGCAGGAGACCGTCTCTTTTGGTGTGCTCGATTTATC 2040
Db 33637 TATGAGACTGCAAAACGAAGGGTTGCAGGAGACCGTCTCTTTTGGTGTGCTCGATTTATC 33696
QY 2041 TAACTTCTTCCATAAGATAGTACAAAAACAACGCGGGGTTTCGCCATTTGAGTGGCGG 2100
Db 33697 TAACTTCTTCCATAAGATAGTACAAAAACAACGCGGGGTTTCGCCATTTGAGTGGCGG 33756
QY 2101 TTATGTCTATAGGAGGAAACCTACATCTTGTTCAGATATAGATTTAGTCTCTCGATTTTG 2160
Db 33757 TTATGTCTATAGGAGGAAACCTACATCTTGTTCAGATATAGATTTAGTCTCTCGATTTTG 33816
QY 2161 TCAGCTCTTTTGAAGAGATAGAGACTTCTTTAGCTTAAAGAAATC-AAGGTACAGTCTTACG 2219
Db 33817 TCAGCTCTTTTGAAGAGATAGAGACTTCTTTAGCTTAAAGAAATCAGAGGTACAGTCTACG 33876
QY 2220 GAGGAACTCTCTANTACAGACCAAGAAACCTATATCTCTCTCTTCCCTTGCACAACTACGGC 2279
Db 33877 GAGGAACTCTCTANTACAGACCAAGAAACCTATATCTCTCTCTTCCCTTGCACAACTACGGC 33936
QY 2280 CTTGTTTGGTGTCTTATGTTCTCTACAGATTCCTGTTCTCTCTTTTTCAGGAAACCTTAGCT 2339
Db 33937 CTTGTTTGGTGTCTTATGTTCTCTACAGATTCCTGTTCTCTCTTTTTCAGGAAACCTTAGCT 33996
QY 2340 ACACCCATACGGATAACGATCTGAAAAACCAAGATATACAAATATCCTACTGTTTAAAGGAA 2399
Db 33997 ACACCCATACGGATAACGATCTGAAAAACCAAGATATACAAATATCCTACTGTTTAAAGGAA 34056
QY 2400 GCTGGGGGAATGATGATTTGCGCTTTTGAATTCGGTGGAGAGCTCCGATTTGCTTAGATG 2459
Db 34057 GCTGGGGGAATGATGATTTGCGCTTTTGAATTCGGTGGAGAGCTCCGATTTGCTTAGATG 34116
QY 2460 AAGATCTCTATTTGAGCAGTACATCCCTTCAATGAAATTCAGATTTGCTATGACATC 2519
Db 34117 AAGATCTCTATTTGAGCAGTACATCCCTTCAATGAAATTCAGATTTGCTATGACATC 34176
QY 2520 AGGAAGTTTAAAGAAACAGGGAACAGAAAGCTCGTGAATTTGGAAGTAGCCGCTTTGTGA 2579
Db 34177 AGGAAGTTTAAAGAAACAGGGAACAGAAAGCTCGTGAATTTGGAAGTAGCCGCTTTGTGA 34236
QY 2580 ATCTTGCCTTACTCTATTCGGATTCGGATTTGATAAGGAATCAGATGCCAAGATGCAACGT 2639
Db 34237 ATCTTGCCTTACTCTATTCGGATTCGGATTTGATAAGGAATCAGATGCCAAGATGCAACGT 34296
QY 2640 ACAATCTACTCTTGGTTTACTGTGGATCTTGTTCGTAGTAACCCGACTGTACGACAA 2699
Db 34297 ACAATCTACTCTTGGTTTACTGTGGATCTTGTTCGTAGTAACCCGACTGTACGACAA 34356
QY 2700 CACTGGAATTAGCGGTGATTTCTTGGAAAAACCTTCGTTACGAATTTGGCAAGACAAAGCTT 2759


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Db 1261 CCCGAGCGTATCGCTCTTTAGTCCCTAATAGCTTATGGAATCATTTATAGATATTAGC 1320
QY 1967 TCTCTCCATATCTATGAGACTGCAACGAAAGGGTTGAGGAGACCGTCTTTTGG 2026
Db 1321 TCTCTCCATATCTATGAGACTGCAACGAAAGGGTTGAGGAGACCGTCTTTTGG 1380
QY 2027 TGTCTCGATTATCTAACTTCTTCCATAAGATAGTACAAAACACGACGCGGTTTCG 2086
Db 1381 TGTCTCGATTATCTAACTTCTTCCATAAGATAGTACAAAACACGACGCGGTTTCG 1440
QY 2087 CATTTAGTGGCGGTTATGTCTATGAGGAGAAACCTACATATCTTGTTCAGATAAGATTCTT 2146
Db 1441 CATTTAGTGGCGGTTATGTCTATGAGGAGAAACCTACATATCTTGTTCAGATAAGATTCTT 1500
QY 2147 AGTCTGCATTTTGTCTAGCTCTTTTGAAGAGATAGAGACTACTTTGTAGCTAAGATCAA 2206
Db 1501 AGTCTGCATTTTGTCTAGCTCTTTTGAAGAGATAGAGACTACTTTGTAGCTAAGATCAA 1560
QY 2207 GGTACAGTCTACGAGGAACCTCTCTATTACCAGCACAAACCAACCTATATCTCTCTTCC 2266
Db 1561 GGTACAGTCTACGAGGAACCTCTCTATTACCAGCACAAACCAACCTATATCTCTCTTCC 1620
QY 2267 TGCAAACTACGCGCTTGTTCGTGTCTTATGTTCCTACAGAGATTCCTGTCTCTTTTCA 2326
Db 1621 TGCAAACTACGCGCTTGTTCGTGTCTTATGTTCCTACAGAGATTCCTGTCTCTTTTCA 1680
QY 2327 GGAACCTTAGCTACACCCATACGGATAACGATCTGAAACCAACCAAGTATACAAATATCCT 2386
Db 1681 GGAACCTTAGCTACACCCATACGGATAACGATCTGAAACCAACCAAGTATACAAATATCCT 1740
QY 2387 ACTGTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGAAGAGCTCCG 2446
Db 1741 ACTGTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGAAGAGCTCCG 1800
QY 2447 ATTTGCTTAGAAGTGTCTTATTTGAGCAGTACATGCGCCCTTCATGAAATTCGAGTTT 2506
Db 1801 ATTTGCTTAGAAGTGTCTTATTTGAGCAGTACATGCGCCCTTCATGAAATTCGAGTTT 1860
QY 2507 GTCTNTGCATACAGNAGGTTTTTAAGAACAGGGAACAGAGCTCGTAATTTGAAAT 2566
Db 1861 GTCTNTGCATACAGNAGGTTTTTAAGAACAGGGAACAGAGCTCGTAATTTGAAAT 1920
QY 2567 AGCGGCTCTTGTGAATCTTGCCTTACCTATCGGATCGATTTCGATAGGAATCAGACTGC 2626
Db 1921 AGCGGCTCTTGTGAATCTTGCCTTACCTATCGGATCGATTTCGATAGGAATCAGACTGC 1980
QY 2627 CAAGATGCAACGTAACATCTAACTCTTTGGTTATCTGTGGATCTTGTTCGTAGTAACCCC 2686
Db 1981 CAAGATGCAACGTAACATCTAACTCTTGGTTATCTGTGGATCTTGTTCGTAGTAACCCC 2040
QY 2687 GACTGTACGACACACTCGGAATTTAGCGGTGATCTTGGAAACCTTCGGTACGAATTTG 2746
Db 2041 GACTGTACGACACACTCGGAATTTAGCGGTGATCTTGGAAACCTTCGGTACGAATTTG 2100
QY 2747 GCAAGCAAGCTTTAGTCCCTTCGTGCAAGGAACCAATTTTGTCTTAACTCAAAATTTGAA 2806
Db 2101 GCAAGCAAGCTTTAGTCCCTTCGTGCAAGGAACCAATTTTGTCTTAACTCAAAATTTGAA 2160
QY 2807 GCCTTTAGCCAAATTTCTTTTGAATTCGTGGGTCATCTCGCAATTAACAATAGTAGACTTA 2866
Db 2161 GCCTTTAGCCAAATTTCTTTTGAATTCGTGGGTCATCTCGCAATTAACAATAGTAGACTTA 2220
QY 2867 GGAGCAAAATACCAATTTCTAA 2887
Db 2221 GGAGCAAAATACCAATTTCTAA 2241
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RESULT 4

US-09-738-269-56

; Sequence 56, Application US/09738269

; Publication No. US20030185848A1

; GENERAL INFORMATION:

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; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
; US-09-738-269-56
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Query Match 18.2%; Score 546.6; DB 10; Length 2781;
Best Local Similarity 53.7%; Pred. No. 6.2e-144;
Matches 1390; Conservative 0; Mismatches 1134; Indels 63; Gaps 10;

QY 328 TTTTAAACAACATAAGGCGAATTTGACTTTCACAGGTAAACGGAACCTCTCTATTGTTCCA 387
Db 231 TTTTGTTCAGACTGCAGACAACCTAACTTTCAAAGGAACAACCATAGCTTATCCATAAC 290
QY 388 AACGTTGGATGCGAGGACTGTAGCAGGGGCTGCTGTTAAACAGCAGCGTGGTAGATAATC 447
Db 291 GAACGGGAATGCGGAGCTAATCC---TGCGGGAATTAACGTTAAACACTCCGATAAGAT 347
QY 448 TACCACCTTTATAGGGTTTTTCTTCGCTATCTTTATTTGCGTCTCTCTGGAAGTTTCGATAAC 507
Db 348 TCCTTACGCTCAGAGATTTTCTTAAGTTGAGCTTTAAGAAATGCCATCTCTCTCTAGTGAA 407
QY 508 TACCGGCAAAAGGAGCCGTAGCTGCTCTACGGGTAGCTTGAGTTTGACAAAAAATGTCAG 567
Db 408 TACTGAAAAAGGGC---TATGAAATCCGGAGGAGCATTAACCTTAGCGAATAATGCCAG 464
QY 568 TTTGCTCTTCAGCAAAAACHTTTCAACGGATATGCGGTGCTATCACCGCAAAAACCTCT 627
Db 465 TATTCTGTTTGAATCAGAACTATTCCGCTGAGAATGTTGGAGCCATCTCTTTGCAAGCTTT 524
QY 628 TTCATTAAACAGGAGCTACAAATGTCAGCTCTGTTTCTGAAAAATACCTCTCAAGAAAGG 687
Db 525 TTCTCTAACCGGCTCGAGCAAGAAATCAGCTTCAACACTACTCTACTCGGAAAAAAGG 584
QY 688 CGAGGCATTCAGACTTCGATGCCCTTACCATTAATGGAACCAAGGGGAAGTCTCTTT 747
Db 585 TGGAGCGATTGCTGCTACGGGAATAGCTCATCTTCGGACAACCAAGGCACAAATCAGATT 644
QY 748 TTCTGACAACTACTCTTCGGAATTCGAGCTGCAATTTTACAGAACCTTCGGTGACTAT 807
Db 645 TTCTGGAACACACTGCTGTGAATTTCTGGGAGCAGTATATTTCAGAACTTCTATGACAT 704
QY 808 TTCTTAATATGCTAAAGTTTCTTATTTGACATAAAGTCAAGGTCAGAGGAGCTCTCTCAAC 867
Db 705 TGCAAGTAACAACAGTTGCTTTTACCAACAATGCTGTTTCCGGTTCATCT----- 756
QY 868 AACGGGGATATGCTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACTAAGT 927
Db 757 -----GATGGTTGCGGTGGAGCTATCCATTTAGCAAAAACAGGTTTCAGCACCGACCT 809
QY 928 CACCCTCCTGGAATCAGATGTTACTCTTCAGCAACAATACATCGACAACAGCGGAGG 987
Db 810 TACTATAAGAGATACAAAAGTCTTGATTTTGGAGAAAAATACTTCTTCAGCAAAAAGTGG 869
QY 988 AGCTATCTATGTGAAAAAGCTCGAACTGCTTCGGAGGACTTTACCTTATTCAGTAGAAA 1047
Db 870 AGCGATTTACCGATAAATCAATTTGATCTCTGTTGGGCTTACGGCATTTTATCAATAA 929
QY 1048 TAGTGTCAATGGAGGTACAGCTCTCTAAAGGTGGAGCCATAGCTATATCGAAGATAGTGGGA 1107
Db 930 CAAAGTTACCCATGCTACA---CCTAAGGTGGAGCTATTGGTATTGCTGCCAATGAGA 986
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QY	1108	ATTGAGTTTATCGCCGATAGTGGTGACATTGCTTTTTAGGAA---TACAGTCACTTC	1164
Db	987	ATGTAGCTTAACCGCTGAACATGGGATAATTACTTTTGATAATAAAGCTGATGCCACACA	1046
QY	1165	TACTACTCTCGGGAGCAATAGAGTAGTAGTACGATTAGGAACGAGTGCAAGATGACAGC	1224
Db	1047	AGACAATGCTACRATAAAAAAGAAATGCCATTAACATTGAAGGCAATGGTAAATTCGTCAA	1106
QY	1225	TTTTCGGTTCTGCTCGTAGAGCCACTACTTCTATGATCCCATAACTACACGATCATC	1284
Db	1107	CTTAGCTGACGGTCTCGAAAGAGATTCTTTCTATGATCCATCACAGTTG-----	1159
QY	1285	CACAACAGTTACAGATGCTCTTAAAGTTAATAGAGACTCCGGCAGATTCTGCATCAATA	1344
Db	1160	-----AAGGTAATGCTGCTGATCTTCTCACTTTGGAATAAAGCTGAGGGTGATAAAACGTA	1214
QY	1345	TACAGGGAACATCATCTTCCAGAGAAAAAGTTATCAGACACAGAGCCCGCAGATTCTAA	1404
Db	1215	TAATGGAGAAATTAATTTTTTCAGAGAAAAAGCTCACTGAAGACAAGCTGCTGTGCGGA	1274
QY	1405	AAATCTTACTTCGAAGCTACTACAGCCTGTAACCTCTTTTCAGGAGGTACTCTATCTTTAA	1464
Db	1275	TAACCTAAGACAACATTTACAGCCCTATCACTTTAGCTGCTGGTGAACCTTGTGTACG	1334
QY	1465	ACATGGAGTGACTCTGAGACTCAGGCAATCACTCAACAGCGAGATTCTCGTCTCGAAAT	1524
Db	1335	CAGCGGTGTGAAGTAGAAGCAAAAAACAGTCGTGCAAAACAGCAGGATCTTTGATTTCTGAT	1394
QY	1525	GGAGTGAAGTAAGTACTCTA---GNAAGCTGCTGATCTAGCACCATAACAAATTTGGTCAT	1581
Db	1395	GGATGCAAGCAAAAGTTATCCGCAAAAAACAGAGATGCTACAGTAAGTCTGGCTAT	1454
QY	1582	TAAATCAGTTCTATAGACGGTCAAAAGAGGCAAAAAATAGAAACCAAGCTACGTCAAA	1641
Db	1455	TAATCCGAATACCTTAGATGGAAAAAATTCGCGTAGTCGATCCGTTGCTGCTGGAA	1514
QY	1642	AAATCTGACTTTTATCTGAAACCATCACTTTATTGGAACCGACGGCAAGTTTATGAAAA	1701
Db	1515	GAATGTCACTTTATCAGGTGCTATTGGCGTTATTGATCTTACAGGGAAGTTTATGAAAA	1574
QY	1702	TCATAGTTTAAAGAAATCCTCAGTCTCAGACATCTTAGAGCTCAAAAGCTCTCGAACTGT	1761
Db	1575	CCATAGCTAAATGATAGTTAGCTTTAGAGGAATTCAACTTTCTGGGAAAGTTTCGGT	1634
QY	1762	AACAAGCACCGCAGTGAAGTCCAGATCCTATAATGGGTGAGAAATTCATTACGGCTATCA	1821
Db	1635	GACAAACCAACGTGCTAGTCAATGTTTGGTGTGTTGCTGAACCCCATATGTTATCA	1694
QY	1822	GGGAAC-----TTGGGGCCCAATGTTTGGGGGACAGGGGCTTCTAGCACTGC	1869
Db	1695	AGGAACTGGTCTCTCAGTTGGGTCAAAGATAATAACTCTGATCCTAAAAACAAACAGC	1754
QY	1870	AACCTTCAACTGGACTAAACCTGGCTATATTCCTTAATCCGAGGGTATCGGCTCTTTAGT	1929
Db	1755	AATCTTACCTGGAAATAAACAGAGATATGTTCAAATCTTGAAGCTGCTCGCTAGT	1814
QY	1930	CCCTAATAGCTTATGGAATGCATTTATAGATATTAGTCTCTCCATTATCTTATGGAGAC	1989
Db	1815	ACTCAATAGCTTTGGGATCCTTTATAGATTTACGTTCTATTCAAGATGCTTTGGAAAG	1874
QY	1990	TGCAAAACGAAGGTTGC---AGGGAGACCGTCTTTTGGTGTGCTCGATATCTACATT	2046
Db	1875	TAGTGTGATAGTATCTTTGAGACACGTGCGTGGTGTGTTGGGTCTCTCGAATTTGGGAAC	1934
QY	2047	CTTCCATAGGATAGTACAAAAACCAACGCGGGTTTCGCCATTTAGTGCGCGTTATGT	2106
Db	1935	CTTCCATAAGATCGAATGCTGAAATTCGCAAAATTCGTCATATCAGTTCCGGATATGT	1994
QY	2107	CATAGAGGAACCTACATACCTGTTGATAGAAATCTTAGTGCTGATTTGTTCAGCT	2166
Db	1995	GTTAGAGGCCAACAAATACTCGAGAGAGATTTCTCTTAGTGTGGCTTTCTGTAGTT	2054

QY	2167	CTTTGGAAGAGATAGAGACTACTTTTGTAGCTAAGAAATCAAGGTACAGTCTACGGAGAAC	2222
DB	2055	ATTTCGCAAAAGATAAAGACTACCTTGTGAAGCAGACCGCGCAAAACCTCTATGCGGGTTC	2114
QY	2227	TCCTATATTACCAGCA-----CAACGAAACCTATATCTCTCTCTTGTGCAAACTACGGCC	2280
DB	2115	TGTAATATTATCAGCATGTGAGCAAGTTTGATGATCTCACCGGGTTATTATATGGGCCTAA	2174
QY	2281	TTGTTTCGTTGCTTATCTTCTCCTACAGAGATTCCTGTTTCTCTTTTCAGAGAAACCTTAGCTA	2340
DB	2175	CACGTGTGTTTCAGGGTTTTCTAAAGAGATTCCCTATTCTTCTTGATGCACAAAATACCTA	2234
QY	2341	CACCCATACGGATACGATCTGAAAAACAAGTATACAAATATCTCTACTGTTTAAAGGAAG	2400
DB	2235	TTGGCACACGGCCCAACAACATGACAACGTCCTATACAGACTATCTCTGAAGTGAAGAGTTC	2294
QY	2401	CTGGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGGGAAGAGCTCCGATTTGCTTAGATGA	2460
DB	2295	TTGGGGTAATGATACCTCGGCCTTAACCTTTGTCTACTAGGTACCTATCCGGTATTATTAG	2354
QY	2461	AAGTGCCTCTATTTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTTGTCTATGCACATCA	2520
DB	2355	TTCTTTCTATCTTTTGATAGTTTATGCCCGTTTGCAAAATTACAAGTTCTCTATGGCACCA	2414
QY	2521	GGAAGGTTTTAAAGAACAGGAGAACAGAGCTCGTGAAATTTGGAAAGTAGACCGTCTTGTGAA	2580
DB	2415	AGATGACTTTTAAAGAACCAACACAGAAAGCGCGGTCTTTTGAAGACGACGATCTTCTCAA	2474
QY	2581	TCTTGCCCTTACCATTACGGATCCGATTTGATATAGGAATCAGACTGCCAAGATGCAACGTA	2640
DB	2475	CGTTTCGTACTCTATAGGTATAAAATTTGAGAACTCTCTCTATGGAGAGAAAGTGCTTA	2534
QY	2641	CAATCTAACTCTTGCTTATATCTGTGGATCTGTTCGTAGTAACCCCGACTGTACGACAAC	2700
DB	2535	TGATCTTACACTGATGATATACCTGATGTGTACCGTCATAATCCAGCTGTATGACAGG	2594
QY	2701	ACTCGAAATTAGCGGTGATTCCTGGAAAAACCTTCGGTAGCAAAATTTGGCAGACAAAGCTTT	2760
DB	2595	ATTGGCGATCAATGACGTTTTCTGTTTAAACACACAGCTACGAAATCTTGCTAGACAAAGCTTT	2654
QY	2761	AGTCCTTCGTGCAGGGAACCAATTTTCTGTTTCTTAACTCAAAATTTTGAAGCCTTTAGCCRAAT	2820
DB	2655	CATAGTTGCGCGGGTAAACCAATATGCTCTTAACTCTGGTGTGAGATGTTTCAGTCAGTT	2714
QY	2821	TTCTTTTGAATTCGCTGGGTCTATCTCGCAATTACAATGTAGACTTTAGGAGCAAAATACCA	2880
DB	2715	TGGTTTCGAATTACGAAGCTCTTCAAGAAATTATAACGTAGATCTTGGCGCTAAGGTCG	2774
QY	2881	ATTCTAA 2887	
DB	2775	GTCTAA 2781	

RESULT 5
US-10-023-437-56
; Sequence 56, Application US/10023437
; Publication No. US20020183272A1

/ GENERAL INFORMATION:
 / APPLICANT: JOHNSTON, STEPHEN A.
 / APPLICANT: STENKE-HALE, KATHERINE
 / APPLICANT: SYKES, KATHRYN F.
 / APPLICANT: KALTENBOECK, BERNHARD
 / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF
 / TITLE OF INVENTION: AND/OR POLYPEPTIDE S
 / FILE REFERENCE: UTSD/7360US
 / CURRENT APPLICATION NUMBER: US/10/023,437
 / CURRENT FILING DATE: 2001-12-17
 / PRIOR APPLICATION NUMBER: 60/225,839
 / PRIOR FILING DATE: 2000-12-15
 / NUMBER OF SEQ ID NOS: 69
 / SOFTWARE: PatentIn ver. 2.1
 / SEQ ID NO 56
 / LENGTH: 2781

; APPLICANT: KALTENBOECK, BERNHARD
 ; TITLE OF INVENTION: METHODS AND compositions for Vaccination comprising NUCLEIC ACID
 ; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
 ; TITLE OF INVENTION: METHODS AND compositions for Vaccination comprising NUCLEIC ACID
 ; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA

Db 2235 TTGGCACACGCCCAACATGACAACTGCTATATACAGACTATCTGAAGTGAAGGTTTC 2294
Qy 2401 CTGGGGGATGATAGTTTCGCTTTAGAAATCGGTGGAAGAGCTCCGATTTGCTTAGATGA 2460
Db 2295 TTGGGGATGATGATACCTGGGCTTAACCTTTGCTACTAGCGTACCTATCCCGGTATTTAG 2354
Qy 2461 AAGTCTCTATTTAGAGAGTACATGCCCTTCATGAAATTTGCAATTTGCTATGCAATCA 2520
Db 2355 TTCCTCTATCTTTAGATGATGACCGTTTGCAAAATTTACAAGTTTGTCTATGCGCACCA 2414
Qy 2521 GGAAGGTTTAAAGAACAGGGGAACAGAGCTCGTGAATTTGGAAGTAGCCGCTTTGTGAA 2580
Db 2415 AGATGACTTTAAAGAACCAACACAGAGCGCGGTCTTTTGAAGCAGCGATCTTTCTCAA 2474
Qy 2581 TCTTCCCTTACCTATCGGATCCGATTTGATAAGGAATCAGACTGCGAAGATGCAACGTA 2640
Db 2475 CGTTTCTGTACCTATAGGTATTAATAATTTGAGAACTCTCTATGAGAGAGAGTGTCTTA 2534
Qy 2641 CAATCTAACTCTGTGTTATPACTGTGATCTTGTTCGTAGTAACCCGACTGTACGACAA 2700
Db 2535 TGATCTTACACTGATGATATACCTGATGTGACCGTCATAATCCAAGCTGTATGACAGG 2594
Qy 2701 ACTGGAATACCGGTGATCTTGGAAACCTTCGGTAGCAATTTGGCAAGACAAGCTTTT 2760
Db 2595 ATTGGGATCAATGACGTTTCTCGTTTAAACCAAGCTACCAATCTTGTAGACAAGCTTT 2654
Qy 2761 AGTCTCTCGTGAGGAAACCTTTTGTCTTAACTCAAAATTTTGAAGCCTTTAGCCAAAT 2820
Db 2655 CATAGTTCCGCGGGTAAACCATTTGCCCCTTAACCTCTGCTGTGAGATGTTGAGTCAGT 2714
Qy 2821 TTCTTTTGAATTCGGTGTGATCTGCAATTCGAATTAACATGAGACTTAGAGGCAAAATACCA 2880
Db 2715 TGGTTTCGAATTAACGAAGCTCTTCAAGAAATTTAAGCTAGATCTTGGCGCTAAGTCTGC 2774
Qy 2881 ATTCTAA 2887
Db 2775 GTTCTAA 2781

RESULT 6

US-10-312-273-96
; Sequence 96, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
; PRIORITY FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 96
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-96

Query Match 17.6%; Score 527; DB 16; Length 2787;
Best Local Similarity 52.9%; Pred. No. 2.4e-118;
Matches 1413; Conservative 0; Mismatches 138; Indels 75; Gaps 10;
Qy 247 TGCTGGAACTACCTACCTATTTAAGGGAAATGTCTACTCTAGAAAATATTTCTTGGAACAGG 306
Db 156 TACTGGAATAGACTATATCTCTGACAGGAGATATAACTCTGCAAAACCTTGGGATTCGG- 214
Qy 307 CACGCAATCAAAAAAGCTGTTTAAACAACACTAAGGCGGATTTGACTTTTCAACAGGTAA 366
Db 215 --CAGCTTAAAGGAGGTTGTTTCTGACACTACGGAATCTTTAAGCTTTGCCGTA 272
Qy 367 CGGGAATCTCTATTTGTTCCAAAACGTTGATGACAGGACTGTAGCAGGGGCTGCTTAA 426
Db 273 GGGGTACTCACTTCTTTTAAATATTAAGTCTAGTCTAAGCGCGCAGCACTTTCTGT 332
Qy 427 CAGCAGCGTGTAGATAAATCTACCAAGTTTATAGGGTTTCTTCGCTATCTTTTATTGC 486
Db 333 TACAATCTGATTAATAATCTGTCTGCTAAAGGATTTTCGAGTCTTACTTTCTTAGCGGCC 392
Qy 487 GTCTCTCGAAGTTTCGATAAATCTACCGCAAGAGGCGGTTAGCTGCTCTACGGGTAGCTT 546
Db 393 ATCATCGGTAATCAACACCCCTCAGGAAAGGTCAGTTAAATGTGGAGGGGATC--T 449
Qy 547 GAGTTTGACAAAAATATGTCAGTTTCTCTTCAAGAAAAACTTTTCAACGATAATCGCGG 606
Db 450 TACATTTGATTAACAATGGAATCTATTTTAAACAAGATTAATCTGTAGGAAAAATGGCG 509
Qy 607 TGCTATACCGCAAAAACTCTTTTCAATTAACAGGGACTCAATGTGAGCTCTGTTTCTCA 666
Db 510 AGCAATTTTACCAAGATCTTTCTTGAANAACAGCAGGATCGAATTTCTTTTGAAG 569
Qy 667 AAATA-----CCTCTCAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTAC 717
Db 570 GAATAAATCGAGCGCAACAGGGAAGGTCGGGCTATTGCTGCTACTGCTACTGTAGA 629
Qy 718 CATTAATGGAACCAAGGGAGTCTCTTTTCTGACATATCTTTCGATTTCTGGAGC 777
Db 630 TATTAACAATAACGGCTCTTACCCCTCTCTCGAACATAATTTGCTGAAGCTGCAGTGG 689
Qy 778 TGCAATTTTACAGAAAGCTCGTCTGACTATTTCTAATATGCTAAAGTTTCTCTTTATGA 837
Db 690 AGCTATAATAGCAAGGAACTGTACAAATTAAGGAAATACGCTCTCTTTGATTTTCTGA 749
Qy 838 CAATAAGGTCAAGAGGAGCTCTCAACAACAGGGGATATGTCAAGAGGTGCTATCTG 897
Db 750 AAATAGTGTGAC---AGCGACCGCAGGAATGGAGAGCTCTTCTGAGAGATGCCG--- 802
Qy 898 TGCTTATAAAACTAGTACAGATACTAAGGTCAACCTCACTGGAAATCAGATGTTACTCTT 957
Db 803 -----ATGTTACCATATCTGGAAATCAGATGTAATCTT 836
Qy 958 CAGCAACAATACATCGACAACAGCGGAGGAGCTATCTATGTGAAAAGCTCGAAGTGC 1017
Db 837 CTCAGGAACCAAGCTGTAGCTTAATGGCGGAGCAATTTATGCTAAGAACTTACACTGGC 896
Qy 1018 TTCCGGAGGAC-----TTACCCATATTCAGTGAATAATGTCAATGAGAGGTACAGCTCC 1071
Db 897 TTCCGGGGGGGGGGGTATCTCTTTCTTAAACAATAATAGTCCAAAGTACCAGTCCAGG 956
Qy 1072 TAAAGGTGAGCCATAGCTATCGAAGATAGTGGGAATTTGAGTTTATCCCGGATAGTGG 1131
Db 957 TAAATGGTGGAGCCATTTCTATATCTGCACTGGAGAGTGTAGTCTTTTCAGCAGAAAGCAGG 1016
Qy 1132 TGACATTTGCTTTTAAAGGAATACAGTCACTTCTACTACTCC---TGGGACGAATAGAAG 1188
Db 1017 GGACATTAATCTCAATGGGAATGCCAATGTTGCAACTACACCAAACTACAAAAAGAAA 1076
Qy 1189 TAGTATCGACTTAGGAACAGAGTGCAGAGATGACAGCTTTGCGTTCTGCTGCTAGAGC 1248
Db 1077 TTCTATTGACATAGGATCTTCTGCAAAAGATCAAGAAATTTACGTTGCAATATCTGGGCA 1136
Qy 1249 CATCTACTTCTATGATCCCATTAACACTAGGATCATCCACAACAGATTACAGATGTCTTAAA 1308

1137 CATCTTTTCTACGATCCGATTAAGTCTTAATACGCGCTGCGGATCTTACAGATCTTTAAA 1196
1309 AGTTAATGAGACTCCGACAGATCTGCACTACATATACAGGGAACATCATCTTCAAGG 1368
1197 TCTCAATAAGGCTGATCAGGTAATAGTACAGATTAATAGTGGGTCGATGTTTTCTGG 1256
1369 AGAAAGTTATCAGAGACAGAGCGCGAGATTCTTAAAAATCTTACTTCGAACTACTACA 1428
1257 TGAAGACTCTCTGAAGATGAAGCAAAAGTTGACAGCAAACTCTACTTCTACGCTGAAGCA 1316
1429 GCCTGTAACCTTTTACGAGGTACTCTATCTTTTAAAAATGAGTACTCTGCACTCA 1488
1317 GCCTGTAACCTTAACTCAGGAAATTTAGTACTTAAAAAGTGGTCTCACTCTCGATACGA 1376
1489 GGCATTCACTCAACAGACAGATCTCTCTCGAAATGAGAGCTAGGAACTACTTAGAAC 1548
1377 AGGCTTTACTCAGACCGCGGCTTCTCTGTTATTTAGTATGATGCGGCAACAGTTTAAAGC 1436
1549 ---TGTGTATACAGCAACCAATTTGGTCAATTAACATCAGTTCTATAGACGCTGC 1605
1437 AAGTACAGAGAGCTCACTTTTAAAGGCTTTTCAATTCCTGTAGACTCTTTAGCGAGGG 1496
1606 AAGAGGCAAAATAGAAACCAAGCTACGTCAAAAAATCTGACTTTTATCTGGAACCAT 1665
1497 TAAGAAAGTTGTAAATTTCTGCTCTGAGCAAGTAAAAATGTAGCCCTTTAGTGGTCCGAT 1556
1666 CACTTTATTCGACCGGCGGCTTTTATGAAATCATAGTTTAAAGAACTCTCAGTC 1725
1557 TCTCTTTTGGATACCAAGGAAATGCTTTATGAAATCAGACTTTAGGAAAACTCAAGA 1616
1726 CTACGACATCTTAGAGCTCAAGCTTCTGGAACCTGTAAACAGCACCGAGTACTCCAGA 1785
1617 CTTTTCATTTGTGAGCTCTCTGCTGAGTACTGCAACACTACAGATGTTCCAGCGGT 1676
1786 TCTTAAATGGGTGAGAAATTCATTAACGGCTATCAGGAACTTTGGGCCCCAATTTGTTG 1845
1677 TCTACAGTAGCAACTCTCAGCACTATGGTATCAAGGTACTTGGGGAATGACTTGGGT 1736
1846 GG-----GGACAGGGCTTCTACGCTGCAACCTTCACTGGACTTAAACTGG 1893
1737 TGATGATACCGCAAGCACTCAAAGACTAAGACAGCAGACATAGCTTTGGACCAATACAGG 1796
1894 CTATATTCTTAATCCGAGGCTATCGGCTCTTTAGTCCCTAATAGCTTTATGGAATGACT 1953
1797 CTACCTTCGAATCTTGAGGCTCAAGGACTTTAGTCTCTAATAGCTTTGGGATCTTT 1856
1954 TATAGATATAGCTCTCTCAATTAATCTTATGAGACTGCAACAGAGGTTGAGGAGGA 2013
1857 TCCAGACATCCAAAGCAATTCAGGTGTCTATGAGAGAAAGTGTCTTCACTCTTTGTTCA 1916
2014 CCGTGTCTTTTGGTGTGCTGATTAATCTAATCTTCTCCATAAGGATAGTACAAACACG 2073
1917 TCGAGGCTCTCGGCTGCGGAGTCCCAATTTCTTAGATAAAGATAAGAAAGGGGAAAA 1976
2074 ACAGGCTTTCCGCTTTAGTGGGCTTATGTCATAGAGGAGAAACCTACATATCTTTGTT 2133
1977 ACCAAATACCGTCATAAATCTGGTGAATGCTATCGGAGGTGAGCGCAACTTTGTTTC 2036
2134 AGTAAAGATCTTAGTGTGCTGATTTTGTGAGCTCTTTGGAAGAGATAGACTACTTTGT 2193
2037 TGAAGAACTTAATAGCTTTGCTCTTTGCCAATCTTTGGTGGGATAAGAAATTTCTAGT 2096
2194 AGTAAAGATCAAGGTACAGTCTACGAGGAACTCTCTATTACAGCAACCAACCTTA 2253
2097 CGCTAAATATCACTGATACCTATGAGGAGCTTCTATATCAACAACTTACAGAAATG 2156
2254 TATCTCTCTCTTGCAGAACTACGCGCTTGTGTTGTTCTTATGTTCTCTACAGATTC 2313
2157 TAGTGGGTTTATAGGTTGCTCTTAGATAAA---CTTCTGGCTCTTGGAGTCATAAAC 2213
2314 TGTCTCTTTTACGAAACCTTAGTCTACACCCATCGGATACGATCTGAAACCAAGTA 2373

2214 CCTGGTTTTAGAGGGCAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAGTA 2273
2374 TACAAATATCTCTACTGTTTAAAGGAAGCTGGGGAAATGATAGTTTCGCTTTTGAATTCGG 2433
2274 TACTGCGTATCTCTGAGGTGAAGGTTCTTGGGGAAATAATGCTTTTAAACATGATGTTGGG 2333
2434 TGAAGAGCTCCGATTTGCTTAGATGAAGTGCTCTATTTTGGAGCAGTACATGCCCTTCAT 2493
2334 AGCTTCTTCAATCTTATCTGTAATACCTGCAATGTTTTTGTATACCTATGCTCCATACAT 2393
2494 GAAATTCGAGTTTGTCTATGCACATCAGGAAGGTTTTTAAAGAAACAGGAAGCTCG 2553
2394 CAAACTGAATCTGACCTTATATAGTCAGGACAGCTTCTCGAGAAAGGTACAGAGGAAG 2453
2554 TGAATTTGGAAGTAGCGCTCTTGTGAATCTTGCTTACCTATCGGATTCGATTTGATAA 2613
2454 ATCTTTTGTATGACAGCAACCTCTTCAATTTATCTTGCCTATAGGGGTGAAGTTTGAGAA 2513
2614 GGAATCAGACTGCCAAGATGCAAGTCAATCTTAACCTTTGTTTATCTGTTGATCTGTTGT 2673
2514 GTTCTCTGATGTAAAGACTTTTCTTATGATCTGACTTTTATCCTATGTTCTCTGATCTTAT 2573
2674 TCTAGTAAACCCGACTGTACGACACACACTCGAAATTAGCGGTGATTTCTTGGAAAACTT 2733
2574 CCGCAATGATCCCAATGCACTACAGCACTTGTAAATCAGCGAGCCTCTTTGGGAACTTA 2633
2734 CGGTACGAATTTGCGAAGACAAAGCTTTAGTCTTCTGTCGTCGAGGAAACCAATTTTGTCTTAA 2793
2634 TGCCAATACTTAGCAGCAGACAGCCTTGCAGTGCSTGCGAGGCACTCACTACGCTTCTC 2693
2794 CTCAAATTTTGAAGCCTTTTAGCCAAATTTTCTTTTGAATTCGTTGGGTCACTCTCGCAATTA 2853
2694 TCTATGTTTGAAGTGTCTGCGCAAGTTGCTTTGAAGTTTCGTTGGATCTTACGGATTTA 2753
2854 CAATGTAGACTTAGGAGCAAAATACCAATTTCTA 2886
2754 TAATGTAGATCTTTGGGGTAAAGTTCCAAATTTCTA 2786

RESULT 7

US-10-312-273-18
; Sequence 18, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 18
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-18

US-10-312-273-34									
Query Match 17.4%; Score 523; DB 16; Length 534;									
Best Local Similarity 99.8%; Pred. No. 1e-137;									
Matches 534; Conservative 0; Mismatches 0; Indels 1; Gaps 1;									
QY	101	ATGAAGTCTCTTTCCCAAGTTTGATATTTCTACATTTGCTATTTTCCCTTTGCTATG	160						
DB	1	ATGAAGTCTCTTTCCCAAGTTTGATATTTCTACATTTGCTATTTTCCCTTTGCTATG	60						
QY	161	ATTGCTACGACAGATTTTGGATTCAAGTCGCGATTTTCGATGGGAATAAATGGTAAT	220						
DB	61	ATTGCTACGACAGATTTTGGATTCAAGTCGCGATTTTCGATGGGAATAAATGGTAAT	120						
QY	221	TTTTTCAGTTCGTGAGAGTCAGGACATGCTGGAATCTACCTATTTAAGGGAAATGTC	280						
DB	121	TTTTTCAGTTCGTGAGAGTCAGGAGATGCTGGAATCTACCTACCTATTTAAGGGAAATGTC	180						
QY	281	ACTCTAGAAAATATTTCTGGAACAGGACAGCAATCAGAAAAGCTGTTTAAACAACAT	340						
DB	181	ACTCTAGAAAATATTTCTGGAACAGGACAGCAATCAGAAAAGCTGTTTAAACAACAT	240						
QY	341	AAGGGGATTTGATTTTACAGGTAAACGGAACTCTCTATTTGTTCCAAACGGTGGATGCA	400						
DB	241	AAGGGGATTTGATTTTACAGGTAAACGGAACTCTCTATTTGTTCCAAACGGTGGATGCA	300						
QY	401	GGGACTGTAGCAGGGCTGCTCTTAACAGCAGCGTGGTAGATAATCTTACCACGTTTATA	460						
DB	301	GGGACTGTAGCAGGGCTGCTCTTAACAGCAGCGTGGTAGATAATCTTACCACGTTTATA	360						
QY	461	GGGTTTTCTTCGCTATCTTTTATTCGGTCTCTCGAATTCGATTAATCTTACCGCAAGGA	520						
DB	361	GGGTTTTCTTCGCTATCTTTTATTCGGTCTCTCGAATTCGATTAATCTTACCGCAAGGA	420						
QY	521	GCGTTAGTCTCTACGGTAGCTTGAGTTTGACAAAATATGTCAGTTTCTCTCAGC	580						
DB	421	GCGTTAGTCTCTACGGTAGCTTGAGTTTGACAAAATATGTCAGTTTCTCTCAGC	479						
QY	581	AAAAACTTTTCAACGGATTAATGGCGGTGCTATCACCGCAAAAACCTTTTCAATTA	635						
DB	480	AAAAACTTTTCAACGGATTAATGGCGGTGCTATCACCGCAAAAACCTTTTCAATTA	534						
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US-10-312-273-34									
; Sequence 34, Application US/10312273									
; Publication No. US20040005667A1									
; GENERAL INFORMATION:									
; APPLICANT: CHIRON SPA									
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE									
; FILE REFERENCE: P025035W0									
; CURRENT APPLICATION NUMBER: US/10/312,273									
; CURRENT FILING DATE: 2002-12-20									
; PRIORITY NUMBER: 0016363.4									
; PRIORITY FILING DATE: 2000-07-03									
; PRIORITY APPLICATION NUMBER: 0017047.2									
; PRIORITY FILING DATE: 2000-07-11									
; PRIORITY APPLICATION NUMBER: 0017983.8									
; PRIORITY FILING DATE: 2000-07-21									
; PRIORITY APPLICATION NUMBER: 0019368.0									
; PRIORITY FILING DATE: 2000-08-07									
; PRIORITY APPLICATION NUMBER: 0020440.4									
; PRIORITY FILING DATE: 2000-08-18									
; PRIORITY APPLICATION NUMBER: 0022583.9									
; PRIORITY FILING DATE: 2000-09-14									
; PRIORITY APPLICATION NUMBER: 0027549.5									
; PRIORITY FILING DATE: 2000-11-10									
; PRIORITY APPLICATION NUMBER: 0031706.5									
; PRIORITY FILING DATE: 2000-12-22									
; NUMBER OF SEQ ID NOS: 664									
; SOFTWARE: SeqWin99, version 1.02									
; SEQ ID NO 34									
; LENGTH: 2787									
; TYPE: DNA									
; ORGANISM: Chlamydia pneumoniae									

1251 TCTACTTCTATGATCCATAAAGTACAGGATCATCCCAACAGTTTACAGATGTCCTTAAAG 1310
1142 TCTACTTCTATGATCCATAAAGTACAGGATCATCCCAACAGTTTACAGATGTCCTTAAAGT 1201
1311 TTAATGAGACTCCGGCAGATTTCTGCACTACAATATACAGGAAACATCATCTTACACAGGAG 1370
1202 TAAATGGTCTGACCTTGACAGGAAATCCTGCATATCAAGGAACCATCGTATTTCTGAG 1261
1371 AAAAGTATCAGAGACAGAGCGCAGATTTCTAAAATCTTACTTGAAGCTACTACAGC 1430
1262 AGAAGTCTCGAAGCAGAGAGCTGCAAGAGCTGATATCTCAAATCTACAATTCAGCAAC 1321
1431 CTGTAACTCTTTCAGGAGGTAAGTCTTCTTTAAAACATGAGTACTCTCGAGACTCAGG 1490
1322 CTCTAACTCTTTCGGAGGCAACTCTCTCTTAATCAGAGTCACTCTAGTTGCTAAGT 1381
1491 CATCTACTCAACAGGAGATTTCTGCTCGAAATGAGAGCTAGGAACTACTCTAGAACCTG 1550
1382 CTTTTTCGCAATCTCCGGGCTCTACCTCTCTGATGATGACAGGACCAATTAAGAACCG 1441
1551 CTGATCTAGCACCATAAACAATTTGGTCAATTAACATCAGTTCTATAGACGTTGCAAGA 1610
1442 CTGATGGATCACTATCAATAATCTGTTCTCAATGTAGATTCCTTAAAAGAGACCAAGA 1501
1611 AGCAAAAATAGAAAACCAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTT 1670
1502 AGCTACGCTAAAGCAACACAGCAAGTCAGACAGTCACCTTTATCTGGATCGCTCTCTC 1561
1671 TATTGACCGCAGCGGACGCTTTTATGAAAATCATAGTTTAAAGAAATCTCTAGTCTTACG 1730
1562 TTGTAGATCTCTTCTGAAATGTCTAGAAAGATGTCTCTGGAATGCTCTCTGGAATCAAGTCTTTT 1621
1731 ACATCTTAGAGCTCAAGCTT-----CTGGAATGTAAACAGCAGCAGTCACTCCAG 1784
1622 CTGTCTCACTCTTACTGTGACGACCCCGCAATATTCACATCAACAGACTTAGCTGCTG 1681
1785 ATCCTATAATGGGTGAGAAATTCATTTACGGCTATCAGGAACTTGGGGCCCAATTTGTTT 1844
1682 ATCCCTAGAAAATCCCTATCCATTTGGGGATACNAGGGAATGGGCATTAATCTTGGC 1741
1845 GGGGACAGGGC-----TTCTACGACTGCAACCTTCAACTGACTTAAACTGGCTATA 1898
1742 AAGAGGATACGCGACTAAATCCAAAGCAGCGACTCTTACCTGGACAAAACAGGATACA 1801
1899 TTCTTAATCCGAGCGTATCGGCTCTTGTAGTCCCTTAATAGCTTATGAAATGCAATTTAG 1958
1802 ATCCGAATCTGAGCGTGGGAACTTGTGCTAAACAGCTATGGGGATCCTTTGTTG 1861
1959 ATATTAGCTCTCTCCATTTATCTTATGGAGACTGCAAAACGAAGGTTGCGAGGAGACGGTG 2018
1862 ATGTGCGCTCCATACACAGCTTGTAGCCACTAAAGTACGCCAATCTCAAGAACTCGCG 1921
2019 CTTTTTGGTGTGCTGATTAATCTAACTTTCTTCATAGGATAGTACAAAACAGCAGCG 2078
1922 GCATCTGGTGTGAAGGATCTCGAACTCTTCTCCATAAGATAGCAGCAAGATAAATAAG 1981
2079 GGTTCGCCATTTGAGTGGGTTATGTCATAGAGGAACCTACATCTTGTTCAGATA 2138
1982 GTTTTCGCCACATAGTGAGGTTATGTTGTAGAGCGACTACAACATTAGCTTCTGATA 2041
2139 AGATTTCTTAGTGTGCTATTTGTGCTGCTCTTTCGGAAGATAGAGACTCTTTGTAGCTA 2198
2042 ATCTTATCACTGAGCTTCTGCCAATTTTCGGGAAGATAGAGTCACTTTTAAATA 2101
2199 AGAATCAAGTACAGTCTACGAGGAATCTCTTATTAACGACCAACGAACCTATATCT 2258
2102 AAAATAGAGCTTCTGCTATGAGCTTCTCTCCATCTCCAGCATCTAGCAGCTTGTCTT 2161
2259 CTCTTCTTCAACTACGCGCTTGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2318
2162 CTCCAAGCTTGTAC-----GCTACCTTCTCGATCTGAAAGTGAGCAGCCTGTCC 2212

2319 TCTTTTCAGAAACCTTAGCTACACCATACGATAACGATCTGAAACCAAGTATACAA 2378
2213 TCTTTGATGCTCAGATCAGCTATATCTATAGTAAAAATACTATGAAACCTATACACCC 2272
2379 CATATCTTACTGTTTAAAGGAAGCTGGGGGAATGATAGTTTCGTTTGAATTCG--GTG 2435
2273 AAGCACAAAGGAGAGAGCTCGTGTATATAATCAGCGTTGCGCTCTGGAACCTTGCAGCT 2332
2436 GAAGAGCTCCGATTTGCTTAGATGAAGTCTCTATTTAGAGCAGTACATGCCCTTCATGA 2495
2333 CCTTACACACACTGTTTTAAGCCATGAGGCTCTCTTCCACGCGTATTTTCTTTTCATCA 2392
2496 AATTGCAGTTTGTCTATGCACATCAGAAAGGTTTTAAAGAAC---AGGGAACAGAAAGCTC 2552
2393 AAGTAGAGCTTCGTATACATACACCAAGATAGCTTCAAGAAACGTAATACTACTTGGTAC 2452
2553 GTGAATTTGGAAGTAGCCGCTTTGTGAATCTTCCCTTACCTATCGGATCCGATTTGATA 2612
2453 GATCTTTTCGATAGCGGTGATTTAATTAACGCTCTCTGCGCTATTGGAATTACCTTCGAGA 2512
2613 AGGAATCAGACTGCCAAGATGCAACGTACAACTTAACCTCTTGGTTATCTGTGGAATCTTG 2672
2513 GATCTTCGAAACAGAGCGGTGCTTTACGAAGCTACTGTCATCTACGTTGCCGATGCT 2572
2673 TTCTAGTAAACCCGACTGTACGACCAACTGCGAAATTAGCGGTGATTTCTTGAAACCT 2732
2573 ATGTAAGAACTCTGACTGCACGACAGCTCTCTAATCAACATACCTCGTGGAACCTA 2632
2733 TCGGTAAGAAATTTGGCAAGACAGCTTTAGTCTCTCGTGAGGGAACCAATTTTGTGTTA 2792
2633 CAGGAACGAATCTCTCAAGACAGCTGGTATCGAAGAGCAGGGATCTTTTATGCGCTTCT 2692
2793 ACTCAATTTTGAAGCTTTAGCCATTTTCTTTGAAATGCGTGGTCACTCTCGGAAT 2852
2693 CTCCAATTTGAGGTACAAAGTAACTATCTATGGAATTCGTGGATCTTACGAGCT 2752
2853 ACAATCTAGACTTAGGAGCAAAATACCAATTCATA 2887
2753 ACATCCAGATCTTGGAGGTAGTTCCAGTTCTAA 2787

RESULT 9

US-10-282-122A-18496
; Sequence 18496, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578

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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18496
; LENGTH: 2793
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-18496

Query Match          17.1%; Score 514; DB 13; Length 2793;
Best Local Similarity 52.7%; Pred. No. 1.2e-134;
Matches 1404; Conservative 0; Mismatches 1200; Indels 60; Gaps 11;

QY 250 TGGAACTACCTATTTAAGGGAATGCTCACTCTAGAAATATTCCTGGACAGGCAC 309
DB 162 TGGAACTACCTATTTAAGGGAATGCTCACTCTAGAAATATTCCTGGACAGGCAC 218
QY 310 AGCAATCAAAAAGCTGTTTTAAACAACACTAAGGCGGATTTGACTTTTACAGGTAAACGG 369
DB 219 AGCAATCAAAAAGCTGTTTTAAACAACACTAAGGCGGATTTGACTTTTACAGGTAAACGG 278
QY 370 GAACCTCTATTGTTTCAAAACGGTGGATGACAGGACTGTGAGCAGGGGCTGCTGTTTAAACAG 429
DB 279 ATACTCAATTTCAATCAACACGGTAGATGCGGGTTTCAAGATGAGGAGCTGCGG---CAAG 335
QY 430 GAGCGTGGTAGAATATCAACAGTTTATAGGTTTCTCGCTATCTTTTATTCGCTC 489
DB 336 CACAACCTGCTGATTAAGCCCTTCAACATTCACAGGATTTTCTAACCTTTCTTCAATTCGAGC 395
QY 490 TCTCGAAGTTTGATTAACCTACCGCAAGGAGCGGTAGCTGCTCTACGGGTAGCTTGAG 549
DB 396 TCTCGAAGTTTGATTAACCTACCGCAAGGAGCGGTAGCTGCTCTACGGGTAGCTTGAG 452
QY 550 TTGCAAAAATATGTCAGTTTCTCTTTCAGCAAAAATTTTCAACGG-----ATAA 600
DB 453 TCTTACCGAATATGGAACGATTTCTTTAGCAAAAACGCTCTCAATGAAAGCTAATAACAA 512
QY 601 TGGCGTGTATCACCGCAAAAATCTTTTCAATTAACAGGACTACAAATGTCAGCTCTGTT 560
DB 513 TGGCGGAGGATCACCAAAAACCTTTTCTATTTCTGGGAATACCTCTTCTATTAACCTT 572
QY 661 TTCTGAAATACCTCTCTCAAGAAAGCGGAGCCATTCAGACTTCCGATGCCCTTACCAT 720
DB 573 CACTAGTAATAGCGCAAAAATATAGGTGAGGGATCTATAGCTCTGCGGCTGCAAGTAT 632
QY 721 TACTGAAACCAAGGGAAGTCTCTTTTCTGCAATATCTTCTTGGATCTTGAGCTGC 780
DB 633 TTCAAGAAACACCGGCAAGTCTTTATGAAATATAAGGAGAAACTGGGGGTGGGC 692
QY 781 AATTTTACAGAGCTCGGTGACTATTTCTTAATATGCTAAAGTTTCTTTTATGACAA 840
DB 693 TCTGGGCTTTGAAGCAGCTCTCGATTAATCTCAAAATAGCTCCCTTTCTCTGGA 752
QY 841 TAAGGTACAGGAGGAGCTCTCTCAACACGGGGGATATGTACAGGAGGTGCTATCTGTGC 900
DB 753 CACTGCAACAGATGCTGCAGGCAAG-----GGCGGGGCAATTTATTTG 794
QY 901 TTATAAACTAGTACAGATCTAAGGTACCCCTCACTGGAATCAGATGTTACTCTTACAG 960
DB 795 TGAATAAAACAGGAGAGACTCTACTCTTACTATCTCTGGAATAAAGTCTGACCTTCGC 854
QY 961 CAACAATACATCGACAACAGCGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTC 1020
DB 855 CGAAGACTCTTCAAGTAACTCAAGCGGAGCAATCTGTGCCATGGTCTAGATCTTCCGC 914
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QY 1081 AGCCATAGCTATCGAAGATAGTGGGGAATGAGTTTATCCGCCGATAGTGGTACATGTT 1140
DB 975 CGCTATTGCAATTTGCCGACTCTCGGATCTTTAAGTCTCTCTGCAAAATCAAGGAGACATCAC 1034
QY 1141 CTTTTTAGGGAATACAGTCACTTCTA---TACTCTCTGGGAGCAATAGAAAGTAGTATCGA 1197
DB 1035 GTTCTCTGGACACTCTTAACCTCAACCTCCGCGCAACATCGACACGGAATGCTATCTA 1094
QY 1198 CTTAGGAACGAGTGCAAAAGATGACAGCTTTTGGCTTCTGCTGCTGTGTAGAGCCATCTACTT 1257
DB 1095 CCTGGATCGTCAGCAAAAATTTACGAACTTTAAGGCGAGCCCAAGCCCAATCTATCTATT 1154
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DB 1632 GGTGGTATTCACTGCTGCTACTGCTAGCGATATTTATATCGATGCGCTTCTCACTTC 1691
QY 1786 TCTTATATAGGTGAGAAATTCATTCAGGCTATCAGGAACTTGGGGCCCAATGTTTG 1845
DB 1692 TCCAGTACAACTCCAGAACCTCATTTACGGGTATCAGGACATTTGGAAGCCACTTGGGC 1751
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RESULT 11

US-10-289-762-1/c

; Sequence 1, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Grifais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 1

; LENGTH: 1230025

; TYPE: DNA

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; Patent No. US20020094340A1
; GENERAL INFORMATION:
; APPLICANT: MURDIN, Andrew D.
; APPLICANT: COMEN, Raymond P.
; APPLICANT: WANG, Joe
; APPLICANT: DUNN, Pamela
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: US\$ THEREOF
; FILE REFERENCE: 032931/0216
; CURRENT APPLICATION NUMBER: US/09/452,380
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
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US-09-452-380-1

Query Match 16.9%; Score 506.6; DB 9; Length 3050;
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Qy 417 CTGCTGTTAACAGCAGCGTGGTAGATAAATCTACCACTTTATAGGTTTCTTCGCTAT 476
Db 426 CTGTAGCCAGTACTCTCAGCAGCAGATAAGAACTCTCTCTTTAATGATTTTCTTAGACTCT 485
Qy 477 CTTTATTTGGTCTCTCTGGAAGTTTCGATTAACCTACCGGCAAGAGCGGTAGCTGCTTA 536
Db 486 CTATTATCTCTTCTGCT 545
Qy 537 CGGGTAGCTTGAGTTTGAACAAAAATGTCAAGTTTGTCTCTTTCAGCAAAACTTTTCAACGG 596


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QY 2718 ATTCTTGGAAAACTTCGGTAGCAATTTTGGCAAGACAAAGCTTTAGTCTCTTCGTCAGGGA 2777
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2742 CTAAGTGGATGGCTATGGTACCACTCGACGACAAAGTTTCTGTTCGTGCTCGGA 2801
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2778 ACCATTTTCTTTAACTCAAAATTTTGAAGCTTTTAGCCAAATTTCTTTTGAATTTGGTG 2837
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2802 ACCATTTCCAAGTGAACCCCAACATGCAATCTTCGGTCAATTCGCTTTTGAAGTACGAA 2861
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2838 GGTCACTCCGAATTAACATGTAGACTTAGAGCAAAAATACCAATTTCTA 2886
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2862 GTTCTTCAAGAAATTAATAACAACCTAGGCTCTAAGTTTGTGTTCTA 2910
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-10-324-129-1
; Sequence 1, Application US/10324129
; Publication No. US20030157124A1
; GENERAL INFORMATION:
; APPLICANT: Mordin et al.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
; FILE REFERENCE: 77813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3050
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(2908)
US-10-324-129-1

Query Match 16.9%; Score 506.6; DB 15; Length 3050;
Best local Similarity 51.3%; Pred. No. 1.6e-132;
Matches 1473; Conservative 0; Mismatches 1324; Indels 72; Gaps 10;

QY 66 AATATTAAATCAAAATCAAGTATATTTTACAATGAAGTCTTTCCCAAGTTTG 125
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
66 AATTTAATTTCCCTTGTTCAAAAGTCTTACAATGAAGTCTCTGTCTCTTGGTTGT 125
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 126 TATTTTCTACATTTGCTATTTTCCCTT---TGTCTATGATGTCTACCGACAGTTTGG 182
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
126 TCTTTTCTCAATCCCGCTCTTTTCATCGCTCTCTATAGTCGGCGCAGAGGTGACCTTAG 185
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 183 ATTCAAG---TGGAGTTTCGATGGGAATAAATGTTAATTTTCAAGTCTGAGAGTC 239
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
186 ATAGCAACAATAATAGTATGATGTATGATGATCTAACCGAACTACCTTCACGGTCTTTTCCA 245
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 240 AGGAAGATGCT---GGAACTACCTTACCTATTTAAGGGAATGTCACTCTAGAAAATATTC 296
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
246 CGNAGCTGTGTCGAGGAATCTACCTATTTCTTACCTTCGAGCTATCTTTCAAAATCGAG 305
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 297 CTGGAACAGGCACAGCAATCAAAAAAGCTGTTTTTAAACACACTTAAGGGCGAATTTGACTT 356
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
306 GGGCTTTTAGGAATTCCTTAGCTCAGAGTGTCTTCTTAGAAGCGGGCGCGATCTTACTT 365
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 357 TCACAGTAACGGGAATCTCTATTGTTCCAAAGCGGTGATGCAAGGACTGTAGCAGGG 416
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
366 TCCAAGGAATTAACATGTCATGAAGTTTGCATTTATCAATGCGGGCTCTAGCGCTGGAA 425
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 417 CTGCTGTTAAGCAGCGGTGTAGATAAACTACCAAGTTTATAGGGTTTCTTCGCTAT 476
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
426 CTGTAGCAGTACTCAGCAGCAGATGAATCTTCTTTTATGATTTTCTAGACTCT 485
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 477 CTTTATTGGTCTCTCTGGAAGTTTCGATAACTACCGCAAGGAGCGGTAGCTGTCTTA 536
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 486 CTATTATCTCTTGTCCCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 545
QY 537 CGGGTAGCTTGAGTTTTCAGAAAAAATGTCAGTTTGTCTCTTTCAGCAAAAACTTTTTCACGG 596
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
546 TGGGGAATCTATCTCTAACTGGCAATTTCCCAAAATATATTTTACTCAGAACTTCTCTGTGAG 605
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 597 ATAAATGGCGGTGTATCACCGCAAAAACTCTTTCAATTAACAGGAGCTTCAATGTTCAGCTC 656
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
606 ATAAACGGCGGTGTATCAATACGAAAAAACTCTTTATTTATCAGGAGCATCTCAGTTTGGGA 665
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 657 TGTTTTCTGAAAAATACCTCTCT---CAAAGAAAGCGGAGCCATTTCAGACTTCCGATG 710
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
666 GCTTTTTCGAAACCAAGCCTTTCAGGGGAAGCAAGCGGTGTAGTTTACGCTACAGGAA 725
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 711 CCCTTACCATTTACTGGAACCAAGGGGAAGTCTCTTTTCTGCAATACTTCTTCGATTT 770
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
726 CTATAACTATTCGAGAAACAGCCCTGGGATAGTTTCTCTCTCAAAACCTTAGCGAAAGGAT 785
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 771 CTGGAGCTGCAATTTTACAGAAAGCCTCGGTGACTATTTCTAATAATGCTTAAAGTTTCTCT 830
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
786 CTGGCGGTGTCTGTACAGCACTGACAACTGTTCGATTACAGATAACTTTCAAGTGATCT 845
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 831 TTATTGACAATAAGGTCACAGAGCGAGTCTTCAACAACAGGGGGATATGTCCAGAGGTG 890
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
846 TTGACGGCAATAGTGTCTTGGGAAGCGGCTCAAGCTCAGGGCGGGGCTAT----- 894
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 891 CTATCTGTGCTTATAAACTAGTACAGATACTAAGTTCACCTCACCTGGAATCAGATGT 950
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
895 -----TTGTGCACTACGACAGATAAAACAGTACTTCTTACTGGGAACAAAAACC 944
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 951 TACTCTTTCAGCAACAATACATCGACAACAGCGGAGGAGTATCTATGTGAAAAGGCTCG 1010
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
945 TCTCTTTCACAAATAATACAGCAATTGACATATGGCGAGGCCATCTCTGGACTCAAGTCA 1004
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1011 AACTGGCTTCCGAGAGCTTACCCCTATTTCAGTGAATAATGTCAATFGAGGTACAGTCT 1070
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1005 GTATTTCCGCTGGAGGTCTTACTCTATTTCAAAAGTAAATATCTCAGGAAGTAGCGCCGCT 1064
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1071 ---CTAAGGTGGAGCCATAGCTATCGAGATAGTGGGAATTCAGTTTATCCGCCGATA 1127
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1065 AGGAGAGGAGGAGCGGATCAATATAGCATCTGCTGGGGAACCTGCTCTCTCTGCTACTT 1124
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1128 GTGTCACATGTTCTTTTAGGGAATACAGTCACTTCTACTCTCTGGACCAATAGAA 1187
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1125 CTGAGATATTACTTCAATAACCAAGTCAACCAAGGAGGACACAAAGTACAGAAACG 1184
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1188 GTAGTATCGATAGGAACGAGTGCAAGATGACAGCTTTGGTTCGTCTGTGTGTAGAG 1247
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1185 CAATAAATATCAITGTATAC---CGCTAAAGTCAATCGATACGAGTGTCTACGGGGCAAT 1241
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1248 CCATCTACTTCTATGATCCCATTACTACAGATCATCCACAAGTTTACAGATGTCTTAA 1307
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1242 CTATCTATTTCATGATGCCATCAAAATCCAGAAACCGAGCTTCTACCGACACATTTGA 1301
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1308 AAGTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTTCACAG 1367
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1302 ACTTAACTTTAGCAGATGCGAACAGTGAGTACAGTATGCGGGTGGCAATGTCTTTCTG 1361
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1368 GAGAAAAGTTTATCAGAGACAGAGCGCGAGATTCTTAAATCTTACTTTCGAAAGTACTAC 1427
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1362 GAGAAAAGCTTTCCCTTACAGAAAAAGCAATCGCTGCAAAACGTCACTCTACTATCCGAC 1421
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1428 AGCTGTACTCTTTTTCAGGAGTACTCTATCTTTTAAACATGAGTGTCTTCGAGACTC 1487
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1422 AACCTGAGTATTAGCGCGGGGAGATCTTGTACTTCTGTATGAGTACCGTAACCTTTCA 1481
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1488 AGGCATTCTACTCAACAGGAGATTCTCGTCTCGAAATGAGACGTAGGAACCTACTCTAGAAC 1547
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1482 AGATCTGACTCAAGTCCAGGATCCGCATCTTAATGATGGGGGACCTACACTTAGTG 1541
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1548 CT---GCTGATCTAGCACCAATAAACAATTTGGTCAATTAAACATCAGTCTTATAGAGGTG 1604
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1542 CTAAAGAGGCAAAATCTTTCGCTTAAATGGCTTAGCAGTAAATCTCTCTCTTCTTAGATGAA 1601
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy	1605	CAAGAAGGC	AAAAATG	AGAAACCA	AAGCTAC	GTCAAA	AAAAATCT	GACTTTT	ATCTG	AAACCA	CC	1664	
Db	1602	CCAACAGG	CAGCTTT	AAAAAC	CAGAAGCT	GCAGATA	AAAAATAT	CAGCCTT	ATCGG	AAACGA	1661		
Qy	1665	TCACCTTT	TGGACCG	CAGCGG	CAGCTTT	TATGAA	AAATCAT	GATGTTT	TAAGAA	AAATCCT	CAGT	1724	
Db	1662	TTGCGCTT	ATTGAC	CACGGA	AGGGTCA	TTCTAT	GAGAAATCA	TAACTTT	AAAAAG	TGCTAGTA	1721		
Qy	1725	CCTACGAC	ATCTTAG	AGTCA	-----	AAGCTT	CTGGA	ACTGT	TAAAC	GACACCC	CAG	1775	
Db	1722	CCTATCCT	CTCTTGA	ACTTACC	ACG	CAGGAGC	CAACGG	ACGAT	TACTCT	TGGAGCTC	1781		
Qy	1776	TGACTCAG	ATCCTAT	TAATGG	TGAGAAA	TTCCAT	TACGGT	ATACGG	GAACCT	TGCGG	GC	1835	
Db	1782	TTTCTAC	CCCTGACT	CTTCA	GAACCTCG	AAACCC	ACTACGG	GTATCA	AGGAAA	CTTGG	CAGT	1841	
Qy	1836	CAATTTGT	TTGGG	GACAGGG	GGCTTCT	ACGCTG	CAAGCTT	CAACTG	GACATA	AAACTCG	GC	1895	
Db	1842	TGCTTTGG	CGAAATG	CAACAT	CTCTCA	AAAT	TAGGAG	CACTCA	CTTG	GACCGT	ACAGAT	1901	
Qy	1896	ATATTCCT	TAATCCG	AGCGTAT	CGGCTCT	TTTAGT	CCCTA	TAGCTT	TAGAA	TGCAT	TTTA	1955	
Db	1902	ACAATCCT	AGTCTG	TAGAAA	AAAGTA	ATCTCC	CTCTA	AAATAG	CTTAT	TGGG	AACTTTA	1961	
Qy	1956	TAGATATT	AGCTCT	CTCTC	ATTATCT	TATG	GAGACTG	CAAA	AGGA	AGGTTT	GCAGGAGACC	2015	
Db	1962	TAGATAT	ACGCTCG	ATCAAT	CAGCTTAT	GAAA	CAAGT	CCAGT	TGGG	AGCCTTT	TGAGC	2021	
Qy	2016	GTGCTTTT	TGCTGT	CGATTACT	TAAC	TTCTT	CCAT	TAGG	TAGTAC	AAAA	CACGAC	2075	
Db	2022	GTGAGCT	ATGGCTT	TGAGGA	ATTCG	GAATTTCT	TCTAT	TAGAG	ATCTA	TGCC	CHACCCGCC	2081	
Qy	2076	GCGGTTTC	GCCATTT	GAGTGG	CGGTTAT	GTCA	TAGG	AGGAA	CCCTA	CTATCT	TGTTT	CAG	2135
Db	2082	ATGTTTCC	GGCATAT	CAGCG	GGGGTTAT	GC	ACTAG	GGAT	CACAG	AACTCT	CTCGC	2141	
Qy	2136	ATAGATT	CTAGT	CTGCAT	TTTGT	CAGCTCT	TTT	TGGA	GAGATAG	AGACT	CTTTG	TAG	2195
Db	2142	AGGATCAG	CTTACTTT	TGCTTCT	CGCAGCTCT	TTT	TGCT	TAGAG	ATCG	CAATCAT	ATTAC	2201	
Qy	2196	CTAAGAT	CAAGGTAC	AGTCTAC	GAGGAG	AACTCTCT	ATTAC	CAGC	-----	-----	-----	2240	
Db	2202	GTAAGACC	ACGGAGAT	ACTTAC	CGTG	GCCTCTT	TGTAT	TTCC	ACCAT	CACAG	AGGGCTCT	2261	
Qy	2241	---ACAA	CGAAACCT	ATATCT	CTCTCT	CTTCA	AAACTAC	CGGCC	TTGTT	CGTTG	CTTATG	2297	
Db	2262	TCGACAT	CGCCAA	TTTCTCT	TGGG	AAAAAGCA	ACC	CGAGCT	CCCTG	GGTGCTCT	CTCAG	2321	
Qy	2298	TTCTC	TACAGATT	CTGTCTCT	TTTTC	AGAA	ACCTTAG	CTAC	CCAT	CAGATAC	GC	2357	
Db	2322	TCTCC	CAGATCAT	TTCC	TTAT	TCGT	TCGAT	GCTTAA	ATTCAG	TTATCT	CCATAC	CAGACA	2381
Qy	2358	ATCTGAAA	CCAAAGT	ATAC	ACATATCT	ACTG	TTTAA	GGAAG	CTGGG	GAATCAT	GATG	2417	
Db	2382	ACATGAGA	CATATAT	ATAC	CGATATCT	TATCAT	CAAG	GGTTCT	TGAG	AAAGT	GC	2441	
Qy	2418	TCGCTTT	TAGAA	TTCCG	TGGAAG	AGCTCC	GATTTG	CTTTAG	TAA	AGT	GC	2477	
Db	2442	TCTGTG	CAGATCT	TGGAG	CTAG	CGCTG	CTTTT	TGTTAT	TTCC	GTG	CTC	2501	
Qy	2478	AGTACAT	GCCCTT	CATG	AAATG	CAGT	TTTG	CTAT	G	CATC	AGGAG	2537	
Db	2502	AAGTCGA	ACCTTT	TGTCA	AAAGTA	CAGT	ATATCT	ATG	CGG	CA	CTT	2561	
Qy	2538	AGG	GAACAGA	AGCTCG	TG	GAATTT	TGGA	AGTAG	CCGCTCT	TG	GAATCT	2597	
Db	2562	GTCATG	CTGA	AGGAC	CGCTT	CAAT	TAAG	CGAG	CTTAT	CA	CGTAG	2621	
Qy	2598	GGATCC	GAATTT	GAT	TAAG	GAATC	AGAT	TCG	CCGAAG	ATG	CAAGT	2657	
Db	2622	CGCTC	ACCTCT	CGAA	AGAG	ACTCA	AAATC	CAGAAA	AGG	AACTT	ACG	2681	

RESULT 14

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US-10-282-122A-18495
; Sequence 18495, Application US/10282122A
; Publication No. US2040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18495
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-18495

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Query Match 16.8%; Score 503.6; DB 13; Length 2811;
Best Local Similarity 51.4%; Pred. NO. 1.1e-131;
Matches 1458; Conservative 0; Mismatches 1304; Indels 72; Gaps 10;
101 ATGAAGCTCTCTTCCCAAGTCTGATTTTCTACATTGCTATTTCCTCTT---TGCT 157

1 ATGAAGTCCTCTGTCTCTGTTGGTTGTTCTTTCTTCTCAATCCCGCTCTTTTCATCGCTCTCT 60
158 ATGATTGCTACCGAGACAGTTTGGATTCAAG---TGGAGATTTCGATGGGAATAAAAT 214
61 ATAGTCGCGGACAGAGTGACCTTAGATAGCAGCAATAATAGCTATGATGATCTAAACGGA 120
215 GGTAAATTTTTCAGTTCGTGAGAGTCAGGAAGTCT--GGAAGTACCTACCTATTATTAAG 271
121 ACTACTTCAAGGTCTTTTCCACTACGACGCTGCTGAGGAACCTACTATTCTTCTTACTT 180
272 GGAATATGTCACCTAGAAATATTTCTGGAACAGGCACAGCAATCAAAAGAGCTGTTTT 331
181 TCCGACGTATCTTTTCAAAATGACGGGCTTTAGGAATTCCTTAGCTCAGGATGCTC 240
332 AACACACTAAGGGCATTTGACTTTTCAAGGTAAACGGGAACCTCTATTGTTTCCAAAG 391
241 CTAGAAGCGGGCGGCGACTTTACTTTTCCAAAGGAATCAACATGCATCTGAAGTTTGCATTT 300
392 GTGGATGCAGGACTGTAGCAGGGGCTGTGTTAAACAGCAGCGTGGTAGATAAATCTACC 451
301 ATCAATGCGGGCTTAGCGCTGGAACCTGTAGCCAGTACCTCAGCAGCAGATAGAATCTT 360
452 ACGTTTATAGGGTTTCTTCGCTATCTTTTATTTGCGTCTCTCGAAAGTTCGATAACTACC 511
361 CTCCTTAAATGATTTTCTAGACTCTCTATTATCTCTGTCCCTCTCTTCTCTCTCTCT 420
512 GGCAAAGAGCGGTAGTCTCTACGGGTAGCTTGAAGTTTGAACAAAATGTCAGTTTG 571
421 ACTGSCAATGTCTTTAAATCTGTGGGAATCTATCTCTAACTGSCAATCTCCAAAT 480
572 CTCCTCAGCAAAATCTTTCAACGGATAATGGGGTGTATCAACCGCAAAATCTTTTCA 631
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632 TTAAACGGGACTCAATGTCAAGTCTGTGTTTCTGAAAATACCTCTCT-----CAAGAAA 685
541 TTATCAGGACATCTCAGTTTGGAGCTTTTCAGAAACCAAGCTTTCACAGGGAAGCAA 600
686 GCGGAGCCATTCAGACTTCGATGCGCTTACCAATTAAGTCAAGGAGGAGGAGTCTCT 745
601 GCGGCTGTAGTTTACGCTACAGGAATATAACTATCGAGAACAGCCCTGGGATAGTTTC 660
746 TTTTCTGACAAATCTCTTCGGAATCTGAGCTGCAATTTTACAGAAAGCTCGTGACT 805
661 TTTCTCATAAAGCTAGGAAAGGATCTGGGGTGTCTCTGACGACTGACAACTGTTCG 720
806 ATTTCTAATAATGCTAAAGTTTCTTTATTTGCAATAAGGTCAAGGAGGAGTCTCTCA 865
721 ATTACAGATAAATTTCAAGTGATCTTTGACGGCAATAGTGTGGAAGCGGCTCAAGCT 780
866 ACAACGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACTAAG 925
781 CAGGGCGGGCTAT-----TTGTTGCACTACGACAGATAAAACA 819
926 GTCAACCTCTACTGAAATCAGATGTTACTCTTCAGCAACAATACATCGACAACAGCGGA 985
820 GTGACTTTACTGGGAACAAAACCTCTCTTTTCAAAATATACAGCAATTCACATATGGC 879
986 GGAGCTATCTATGTGAAAAAGCTCGAATCGCTTTCGGGAGGACTTACCTTATTCAGTAGA 1045
880 GGAGCCATCTCTGACTCAAGTTCAGTATTTCCGCTGGAGTCTCTCTCTATTTCAAAGT 939
1046 AATAGTGTCAATGGAGGTACAGTCT---CTAAAGGTGGAGCCATAGTATCGAAGATAGT 1102
940 AATATCTCAGGAAGTAGCGCGGTTCAGGAGGAGGAGGAGCGATCAATATAGCATCTGCT 999
1103 GGGGAATTGAGTTTATCCCGCGAGTAGTGTGACATGTTCTTTTATAGGGAATACAGTCACT 1162
1000 GGGGAAGTCTCTCTCTGCTACTCTGAGATATTTACCTTCAATACCAACCAAGTCAAC 1059
1163 TCTACTACTCTCGGACGAATAGAGTAGTATCGACTTTAGGAACGAGGTGCAAGATGACA 1222
1060 AACGGAAGCACAAAGTACAGAAACGCAATAAATATCATTTGATACC---GCTAAAGTCACA 1116

1223 GCTTTGCGTTCTGCTCGTAGAGCACTACTTCTTATGATCCCATAACTACAGGATCA 1282
1117 TCGATACGAGCTGCTACGGGCAATCTAICTATTCTATGATCCCATCAAAATCCAGGA 1176
1283 TCCACAACAGTTTACAGATGCTCTTAAAGTTAATGAGACTCCGGCAGATTCTGCACTACAA 1342
1177 ACCGAGCTTCTACCGACACATTGAACTTAAACTTAGCAGATCGGAACAGTGAATCGAG 1236
1343 TATACAGGGAACATCATCTTTCACAGGAGAAAGTTATCAGAGACAGAGCGCGCAGATTCT 1402
1237 TATGGGGGTGCGATTGCTCTTTCTGGAGAAAAGCTTTCCCTTACAGAAAAGCAATCGCT 1296
1403 AAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTTCAGGAGTACTCTATCTTTA 1462
1297 GCAAAGCTCACCTCTACTATCCGAACTCTGAGTATTAGCGCGGGAGATCTTGACTT 1356
1463 AAACATGGAGTGACTCTGCAGACTCAGGCATTCACCTCAACAGGCAGATTCTGCTCGAA 1522
1357 CGTGATGGAGTCAACCGTAACCTTTCAAGGATCTGACTCAAAGTCCAGGATCCCGCATCTTA 1416
1523 ATGGAGCTAGGAACCTACTCTAGAACCT---GCTGATACTAGCACCATTAACAATTTGGTC 1579
1417 ATGGATGGGGGAGTACACTTAGTCTAAAGAGGCAAACTTTTCGCTTAATGCTTAGCA 1476
1580 ATTAACATCAGTTTCTATAGACGGTGCAAAAGAGGCAAAATAGAAAACCAAGCTACGTCA 1639
1477 GTAAATCTCTCTCTTTTAGATGGAACCAACAGGAGCTTTAAACACAGAGCTGCAGAT 1536
1640 AAAAATCTGACTTTATCTGGAACCATCACTTTATGGAACCGGACGGGACAGTTTATGAA 1699
1537 AAAAATATCAGCTATCGGGAACGATTGCGCTTATTGACACGGAAGGCTCATTTATGAG 1596
1700 AATCATAGTTTAAAGAACTCTCAGTCTCTACGACATCTTAGAGCTCA-----AGCT 1750
1597 AATCATAACTTAAAGAGTGTAGTACTCTCTCTTTGAACTTACCACCGCAGGAGCC 1656
1751 TCTGGAACTGTAAACAAGCACCGCAGTGAATCCAGATCTCTAATATGGTGAGAAATTCAT 1810
1657 AACGGAACAGATTAATCTGGGAGCTCTTTTACCTGACTCTTCAAGAACCTGAACCCAC 1716
1811 TAGCGCTATCAGGGAACCTTGGGGCCCAATTTGTTGGGGGACAGGGGCTTCTACGACTGCA 1870
1717 TAGCGGTATCAAGGAAACCTGCGAGTTGTCTTGGGCAAAATGCAACATCTCAAAAATAGGA 1776
1871 ACCTTCAACTGGACTAAACCTGCTATATCTCTAAATCCCGAGGCTATCGGCTCTTTAGTC 1930
1777 AGCATCAACTGGACCCGTCACAGGATACATTCCTAGTCTCTGAGAGAAAAGTAATCTCCCT 1836
1931 CCTAATAGCTTATGGAATGCAATTTATAGATATTTAGTCTCTCTCAATTTATTTATGGAGACT 1990
1837 CTAAATAGCTTATGGGAAACCTTTATAGATATACGCTCGATCAATCAGCTTATAGAAC 1896
1991 GCAACGAAAGGTTGACGGAGACCGGTCTTTTGGTGTGCTGGATTATCTAATCTTCTTC 2050
1897 AAGTCCAGTGGGAGCCCTTTTGGCGGTGAGTATGGCTTTCAGGAATGGGAATTTCTTC 1956
2051 CATAGGATAGTACAAAACACGACGGGGTTTTCGCAATTTGAGTGGCGGTATGTCTATA 2110
1957 TATAGGATTTCTATGCCACCCCGCATGGTTTCCGCCATATACGCGGGGTATGCACTA 2016
2111 GGAGGAACCTACATCTCTTTCAGATAAGATTTCTTAGTGTGCTGATTTTGTGCTAGCTCTTT 2170
2017 GGGATCACACAACATCTCTCGGAGGATCAGTTACTTTTGGCTTCTGCCAGCTCTTT 2076
2171 GGAAGGATAGAGACTATTTGTAGCTAAGAACTCAAGGTACAGTCTACGAGGAACCTCTC 2230
2077 GCTAGAGATCGAATCATATTTACAGGTAAAGAACCAAGGAGATCTTACGGTGCCTCTTTG 2136
2231 TATTACAGCA-----CAACGAACCTATATCTCTCTCTCTCTCTGCAAA 2272
2137 TATTTCCACATACAGAAGGGCTCTTCGACATCGCAATTTCTCTGGGGAAGCAACC 2196

QY	1046	AAATAGTGTCAATGGAGGTACAGCTC---CTAAAGGTGGAGCCATAGCTATCGAAGATAGT	1102
Db	940	AAATATCTCAGGAAGTAGCGCGGTTCAGGGAGGAGGAGCGATCAATA TAGCATCTGCT	999
QY	1103	GGGGAATTAGTATTACCGCGGATAGTGGTGACATTTGTCTTTTATGGGAATACAGTCACT	1162
Db	1000	GGGGAATCGCTCTCTCTGTCTACTCTTCGAGATATTACCTTTCAATAACAACCAAGTCAAC	1059
QY	1163	TCTACTACTCCTGGGACGAATAGAAGTAGTATCGACTTAGAAACGAGTGCAAAGATGACA	1222
Db	1060	AACGHRAGCACAGTACAAGAAACGCAATAAATATCATTTGATACC---GCTAAAGTCACA	1116
QY	1223	GCTTTGGTGTCTGCTGTGTAGAGCAATCTACTTTATGATCCCAATACTACAGGATCA	1282
Db	1117	TCGATACGAGTGTCTACGGGCAATCTATCTATTTCCTATGATCCATCACAAAATCCAGGA	1176
QY	1283	TCCACAAACAGTTACAGATGTCCTTAAAGTTAAATGAGACTCCGACGATTCTGCACACTCAA	1342
Db	1177	ACGCGAGCTTCTACCGACACATTTAAACTTTAGCAGATCGGAACAGTGAATCGGAG	1236
QY	1343	TATACAGGGAACATCATCTTTCACAGGAGAAAAGTTATCAGAGACAGAGGCGCGAGATTCT	1402
Db	1237	TATGGGGTGGGATTGTCTTTCTGGAGAAAAGCTTTCCCTACAGAAAAGCAATCGCT	1296
QY	1403	AAAAATCTTACTCGAAGCTACTACAGCCTGTAACTCTTTTCAGAGAGTACTCTATCTTTTA	1462
Db	1297	GCAACGTCACCTCTACTATCCGACAACTCGAGTATTAGCGGGGAGATCTTGTAATT	1356
QY	1463	AAACATGGAGTACTCTGCAGACTCAGGCATTCACTCAACAGGCAGATTCTCGTCTCGAA	1522
Db	1357	CGTGATGGAGTCAACGTTAACTTTCAAGGATCTGACTCAAAAGTCAGGATCCCGCATCTTA	1416
QY	1523	ATGGAAGTGAAGAACTACTCTAGAACTT---GCTGATACTAGCAACCAATAAAATTTGGTC	1579
Db	1417	ATGGATGGGGGACTACACTTAGTGCTAAAAGAGGCAAAATCTTTTCGCTTAATGGCTTAGCA	1476
QY	1580	ATTAACATCAGTTCTATAGACGGTGCAAAAGAGGCAAAAATAGAAACCAAGCTACGTCA	1639
Db	1477	GTAATCTCTCCCTTTTAGATGGAAACCAACAGGCAGCTTTTAAACACAGAAAGCTGCAGAT	1536
QY	1640	AAAAATCTGACTTTATCTGGAACCATCACATTTATTGGACCGGACCGTCTTTATGAA	1699
Db	1537	AAAAATACAGCTATCGGNAACGATTTGGCTTTATTCACAGGAGGGTCAITCTATGAG	1596
QY	1700	AATCATAGTTTATAGAAATCCTCAGTCTCAGACATCTTAGAGTCA-----AAGCT	1750
Db	1597	AATCATAACTTAAAAAGTGTAGTACCTATCTCTCTTTGAACTTACCAACCGCAGGAGCC	1656
QY	1751	TCTGGAACTGTAAACAACACCGAGTGACTCCAGATCCTATTAATGGGTGAGAAATTCAT	1810
Db	1657	AACGGAAACGATTACTCTGGGAGCTCTTTTACCTCTGACTCTTCAAGAACCTGAAACCCAC	1716
QY	1811	TACGGCTATCAGGGAACTTGGGGCCCAATTTGTTTGGGGGACAGGGGCTTCTACGACTGCA	1870
Db	1717	TACGGGTATCAAGGAAACTGSCAGTGTCTTGGGCAATGCAACATCCTCAAAAAATAGGA	1776
QY	1871	ACCTTCAACTGGACTAAACATGGGCTATATTCCTTAATCCGAGCGTATCGGCTCTTTAGTC	1930
Db	1777	AGCATCAACTGGACCGGTACAGGATACATTTCTTAGTCTCTGAGAAAAAGTAATCTCCCT	1836
QY	1931	CCTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCTCCATATCTTATGAGACT	1990
Db	1837	CTAAATAGCTTATGGGNAACCTTTATAGATATACGCTCGATCAATCAGCTTATAGAAACC	1896
QY	1991	GCAACCAAGAGGTTTCAGGGAGACCGTCTTTTGGTGTGCTGGATTATCTAACTTCTTC	2050
Db	1897	AAGTCCAGTGGGGAGCCTTTTGGCGTGGAGTATGGCTTTTTCAGGAATTCGGAATTTCTTC	1956
QY	2051	CATAAGGATAGTACAAAAACACGACGGGGTTTCGCCATTTTGATGGGGTTATGTCAATA	2110
Db	1957	TATAGAGATTCATATGCCACCCGCACTGGTTTCGCCATATACAGCGGGGTTATGCACTA	2016

Qy	2111	GAAGGAAACCTACTACTTGTTCAGATAAGATCTTAGTGCTGATTTTGTACGCTCTTT	217
Db	2017	GGATCACAGCAACACTCTCTGCGAGGATCAGCTTACTTTTGGCTTCTGCCAGCTCTTT	2076
Qy	2171	GAAGAGATAGAGACTACTTTGTAGCTTAAGAAATCAAGGTACAGTCTACGGAGAACTCTC	2230
Db	2077	GCTAGAGATCGCAATCATATTACGGTTAAGAACACGAGATACTTACGGTGCCTCTTTG	2136
Qy	2231	TATTACCAGCA-----CAACGAAACCTATATCTCTCTTTCCTTGCAGAA	2272
Db	2137	TATTTCCACCATACAGAAAGGCTCTTCGACATCGCCAAATTCCTCTGGGAAAGCAACC	2196
Qy	2273	CTACGGCCTTGTTGCTGTCTATGTCTCTACAGAGATTCCTGTTCTCTTTTCAGGAAC	2332
Db	2197	CGAGCTCCCTGGGTGCTCTCTGAGATCTCCGAGATCAATTCCTTTATCGTTTCGATCTAAA	2256
Qy	2333	CTTAGCTACACCATACGGATAACGATCTGAAACCAAGTATACACATATCCTACTGTT	2392
Db	2257	TTCAGTTATCTCATACAGACACCAATGAAGCATATTTATACCGATACTCTATCATC	2316
Qy	2393	AAAGGAAGCTGGGGAAATGATTTTCGCTTTTAAATTCGGTGAAGAGCTCCGATTGTC	2452
Db	2317	AAGGGTCTTTGGAGAAACGATGCTTCTGTGTCAGATCTTGAGAGTAGCCTGCCCTTTGTT	2376
Qy	2453	TTAGATGAAAGTGCTCTATTTTGAGCAGTACATGCCCTTCTATGAAATGCAAGTTTGTCAT	2512
Db	2377	ATTTCCGTTCCGTATCTTCTGAAGAAGTCGAACCTTTGTCAAAGTACAGTATATCTAT	2436
Qy	2513	GCACATCAGGAAGGTTTTTAAAGAACAGGGAAACAGAGCTCGTGAAATTTGGAAGTAGCCGT	2572
Db	2437	GCGCATCAGCAAGACTTCTACGAGCGTCATGCTGAAGAGCGCTTTTCAATAAAAGCGAG	2496
Qy	2573	CTTGTGAACTTTGGCTTACCTATCTGGGATCCGATTTTGATTAAGNATCAGACTGCCAGAT	2632
Db	2497	CTTATCAACGTAGAGATTCCTATAGGCGTCACTTCGAAAAGAGACTCAAAATCAGAAAG	2556
Qy	2633	GCAAGTACAAATCTAATCTTTGGTTATCTGTGGATCTGTTCGTAGTAACCCCGACTGT	2692
Db	2557	GGAACTTACGATCTTACTCTTATGTATATCTCGATGCTTACCGACGCAATCCTAAATGT	2616
Qy	2693	ACGACAACTGCGAAATTAGCGGTGATCTTTGGAAAACTTTCCGTACGAAATTTGGCAAGA	2752
Db	2617	CAAACTTCCCTAATAGCTAGCATGCTAACTGGATGGCTATGGTACCAACCTCGCACGA	2676
Qy	2753	CGAGCTTTAGTCTTCTGTCGAGGGAACCAATTTTGTCTTAACCTCAAAATTTTGAAGCCTTT	2812
Db	2677	CAAGGTTTTTCTGTTCTGTGCTGGAACTATTTCCAGTGAACCCCAACATGGAAATCTTC	2736
Qy	2813	AGCCAAATTTTCTTTTGAATTCGCTGGGTCTATCTCGCAATTTACAATGTAGACTTTAGGACGA	2872
Db	2737	GGTCAATTCGCTTTTGAAGTACGAAGTCTTTCAGGAAATTTATAACAACTTAGGCTCT	2796
Qy	2873	AAATACCAATTTCTA 2886	
Db	2797	AAGTTTGTGTTCTA 2810	

Search completed: August 16, 2004, 21:06:33
Job time : 924 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:07:10 ; Search time 14 seconds
(without alignments)

3451.507 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSSPFKVFSTFAIFPLSM.....FELRGSSRNYNVDLGAKYQF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2058	43.1	528	PM10_CHLPPN	Q9r565 chlamydia p
2	1982	41.5	528	PM10_CHLPPN	Q9z398 chlamydia p
3	1964	41.1	936	PM10_CHLPPN	Q9z898 chlamydia p
4	1936	40.6	930	PM10_CHLPPN	Q9z393 chlamydia p
5	1855	38.9	928	PM11_CHLPPN	Q86164 chlamydia p
6	1573	32.9	841	PM11_CHLPPN	Q9z3a1 chlamydia p
7	1444	30.2	1276	PM16_CHLPPN	Q9z899 chlamydia p
8	1442.5	30.2	922	PM11_CHLPPN	Q9z295 chlamydia p
9	1377.5	28.9	973	PM13_CHLPPN	Q9z896 chlamydia p
10	1120.5	23.5	1013	PM13_CHLPPN	Q84879 chlamydia t
11	1051	22.0	987	PM10_CHLPPN	Q9p145 chlamydia m
12	911	19.1	867	PM11_CHLPPN	Q9p141 chlamydia m
13	863	18.1	878	PM11_CHLPPN	Q84882 chlamydia t
14	685.5	14.4	1609	PM11_CHLPPN	Q9z265 chlamydia p
15	667.5	14.0	978	PM14_CHLPPN	Q9z895 chlamydia p
16	666	14.0	947	PM19_CHLPPN	Q9z813 chlamydia p
17	666	14.0	1723	PM20_CHLPPN	Q9z812 chlamydia p
18	665.5	13.9	946	PM18_CHLPPN	Q9z880 chlamydia p
19	647	13.6	952	PM16_CHLPPN	Q9z882 chlamydia p
20	603.5	12.6	938	PM15_CHLPPN	Q9z883 chlamydia p
21	603	12.6	975	PM15_CHLPPN	Q84417 chlamydia t
22	597	12.5	1016	PM15_CHLPPN	Q84880 chlamydia t
23	594	12.4	980	PM15_CHLPPN	Q9p144 chlamydia m
24	587.5	12.3	976	PM15_CHLPPN	Q9p143 chlamydia m
25	576.5	12.1	1531	PM15_CHLPPN	Q84818 chlamydia t
26	559	11.7	1754	PM15_CHLPPN	Q84418 chlamydia t
27	549	11.5	976	PM15_CHLPPN	Q9p147 chlamydia m
28	548.5	11.5	1672	PM15_CHLPPN	Q9p142 chlamydia m
29	544	11.4	1520	PM15_CHLPPN	Q9p1b0 chlamydia m
30	541.5	11.3	964	PM15_CHLPPN	Q84877 chlamydia t
31	533.5	11.2	1460	PM15_CHLPPN	Q9p141 chlamydia m
32	523	11.0	1770	PM15_CHLPPN	Q84419 chlamydia t
33	490	10.3	1034	PM15_CHLPPN	P38008 chlamydia t

ALIGNMENTS

RESULT 1

ID	PM10_CHLPPN	STANDARD;	PRT;	928 AA.
AC	Q9r565; Q86163; Q9RB64; Q9S6P2;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	Probable outer membrane protein pmp10 precursor (Polymorphic membrane protein 10) (Outer membrane protein 5).			
DE	PM10 OR OMP5 OR CP0303 OR CPB0467.			
GN	Chlamydia pneumoniae (Chlamydia pneumoniae).			
OS	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.			
OX	NCBI_TaxID=83558;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=VR1310;			
RC	MEDLINE=20007584; PubMed=10539856;			
RA	Christiansen G., Boesen T., Hjerne K., Daugaard L., Mygind P.,			
RA	Madsen A.S., Knudsen K., Falk E., Birkelund S.;			
RT	"Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity."			
RL	Am. Heart J. 138:S491-S495(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AR39;			
RC	MEDLINE=20150255; PubMed=10684935;			
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,			
RA	White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,			
RA	Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,			
RA	Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,			
RA	Eisen J., Fraser C.M.;			
RA	"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39."			
RL	Nucleic Acids Res. 28:1397-1406(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=J138;			
RC	MEDLINE=20330349; PubMed=10871362;			
RA	Shitai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,			
RA	Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;			
RT	"Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CW029 from USA."			
RL	Nucleic Acids Res. 28:2311-2314(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=TW-183;			
RA	Geng M.M., Schumacher A., Muehlendorfer I., Bensch K.W., Schaefer K.P.,			
RA	Schneider S., Pohl T., Essig A., Marre R., Melchers K.;			
RT	"The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis."			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 1-914 FROM N.A.			
RC	STRAIN=CWL029/VR-1310;			
RC	MEDLINE=99081766; PubMed=9864239;			
RA	Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;			

Q9z3d6 chlamydia p
Q9p146 chlamydia m
P15921 rickettsia
Q52657 rickettsia
P35828 caulobacter
P47033 saccharomyc
P18305 chilo iride
P35827 campylobact
P96989 r outer mem
Q53020 r outer mem
P40442 saccharomyc
P45508 escherichia

RT "Identification of two novel genes encoding 97- to 99-kilodalton outer
 RL membrane proteins of Chlamydia pneumoniae.";
 CC -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 CC (Potential).
 CC -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 CC -----
 DR EMBL; AJ133034; CAB37071.1; -;
 DR EMBL; AE002192; AAF38160.1; -;
 DR EMBL; AP002546; BAA98657.1; -;
 DR EMBL; AE017158; AAF98398.1; -;
 DR EMBL; AJ001311; CAA04671.1; -;
 DR PIR; G81591; G81591;
 DR PIR; G86546; G86546;
 DR PHCI-2DPAGE; O86163; -;
 DR TIGR; CP0303; -;
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR003368; Chlamydia PMP.
 DR InterPro; IPR00437; Prok lipoprot S.
 DR Pfam; PF02415; Chlamydia PMP; 2.
 DR TIGRFAMs; TIGR01414; autotrans barl; 1.
 DR TIGRFAMs; TIGR01376; POMP_repeat; 6.
 DR Outer membrane; Signal; Multigene family.
 KW SIGNAL
 FT CHAIN 1 25 POTENTIAL.
 FT CHAIN 26 928 PROBABLE OUTER MEMBRANE PROTEIN PMP10.
 FT CONFLICT 305 305 MISSING (IN REF. 4).
 SQ SEQUENCE 928 AA; 97229 MW; 0590D5206A1DD0E1 CRC64;

Query Match 43.1%; Score 2058; DB 1; Length 928;
 Best Local Similarity 46.7%; Pred. No. 3.3e-104;
 Matches 444; Conservative 142; Mismatches 320; Indels 44; Gaps 20;
 1 MKSPKPKVF-STRAIF--PLSMATETVLDSASFQGNK-GNFSVRESQEDAGTYL 55
 1 MKSQSWLVSLSTACFTSCSTVFAETAENTGSPDSFGSTNGTYTKNT--TTGIDYT 58
 56 PKGNVTLENIPTGPAITKSCFNNTKGLTFTNGNSLLFTQVDAGTVAGAVNSVVDK 115
 59 LTGDTITLQNL-GDSAAITKGCPSDTTSLSPAGKGYSLFLNKS-SAEGAAL-SVTYTDK 115
 116 STTFIGFSSLSFIAPGSIIT--GKGAIVCSSTGSLSTKVNLSLFSKNFSTNDGALTA 173
 116 NLSLTGFSSLTFLAAPSSVITTPSGKGAIVKCG-GDLTTFDNNGTILFKQDYCEENGALST 174
 174 KTLSTGTMTGALPENTSS--KKGAIQTSDALITIGNOGEVFSFNTSSDGAALFT 230
 175 KNLSLKNSTGSLSPGKSSATKKGAI CATGTVDTINTAPTFLFSNNIAEAGAINS 234
 231 EASVTISNAKVSDINDKVTGASSSTGDMGGAI CAYKTSPTDKVTLTGQMLFNSNT 290
 235 TGNCTITGNTSLVFSNSVT--ATAG--NGGAL--SGDADVTISGNSQVTFSGNQ 283
 291 STTAGAIVKLELAS--GGLTFLSRNSVNGGTAPKGAIAIEDSGELISLSDGDIIVF 348
 284 AVANGAIYAKKILUASGGGGISFNNIVQGTAGNGAISILAAEGCSLSAEAGDITF 343
 349 LGNTVTSTTP--GTRSSIDLTSAKWTALRGAAGRAIFYDPITTGSSSTVTDVLKVNET 407
 344 NGNAIVATPQTTKNSIDIGSTAKITNLRAISGHSIFYPDITANTAASTDITLNKA 403
 408 PADSMALQYTGNIITFGEKLSSETHADSKNLSKLLQPTVLSGGTISLKHGVTLQTAFTQ 467
 404 DAGNSTDYSGSIVFSGEKLSEDAKVNLTSLKQPVTLTLAGNVLKRGVTLDTKGFTQ 463
 468 QADSRLEMDVGTTLRPA-DTSTINNVLINISSIDGAKKAKIETKATSKNLTLSGTTILLD 526

Db 464 TAGSSVINDAGTTLKASTEETVTLTGLSIPVDSLGEKKVWIAAASAKNVALSGPILLDD 523
 Qy 527 PTGTFYENHSRNPQSYDILELKASGTVTSTAVTDPDPMGEKFHYGYOQTWGPVW--- 582
 Db 524 NQGNAYENHDLGKTQDFSVQLSALGTATTDDVPAVTPVATPHYGYOQTWGTW-VTVDDT 582
 Qy 583 -GTGASTTATNTKTYIPNPERIGSLVPSNLMNAPIDISLHYLMETANEGLQGDRAF 641
 Db 583 ASTPKTKTATLAWNTGYLPNPERQGPLVPSNLWGSFSDIAIOGVIERALSALTLCSDRGF 642
 Qy 642 WCAGLSNFFHDSYKTRRGPRLSGYVIGNMLHTCSKILSAACQIFGRDRDYFVAKN 701
 Db 643 WAAGYANFLDKDKGKKRKYRKHSGGYAIGAAQTCSENLSFPAFCQFLGSKDKFLVAKN 702
 Qy 702 QGVTVGGTLYYQHNETYISLPCKLRPCSLSVVP---TEIPVLFSNLSYVTHDNDLKTKY 758
 Db 703 HTDIYAGAFYIQH----ITECSGFIGCLLDKLPWSHKLPLVLEQLAYSHVNDLKTKY 758
 Qy 759 TTYPTVKGWNGDSFALEFGGRAPICLDESALFEQYMPMKLQFYVAHQEGFKEGTEAR 818
 Db 759 TAYPEVKGWGNNAFNMMLGASSHSYPEYLHCFTDYAFYIKILNTYIRQDSFSEKGTGR 818
 Qy 819 EFGSRVLNLPALPIGIRFDKESDCODATYNLTGLTYVDLVRSPDCTTLRISGDSWTF 878
 Db 819 SFDDSNLFLNLSLPIGVKFEKFCDFDNDYDUTLSYVPLIRNDPKCTTALVISGASWTF 878
 Qy 879 GTNLARQALVLRAGNHFCSNFSAFQSFELRGSSRNYNVDLGAKYQF 928
 Db 879 ANNLRARQALVLRAGSHYAFSPMFEVLGQFVEVRGSSRIYNVDLGKQF 928
 RESULT 2
 PMP9 CHLPN STANDARD; PRT; 928 AA.
 ID PMP9 CHLPN STANDARD; PRT; 928 AA.
 AC Q92398;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable outer membrane protein pmp9 precursor (Polymorphic membrane
 DE protein 9) (Outer membrane protein 10).
 GN PMP9 OR OMP10 OR CPN0447 OR CP0306 OR CPB0464.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydia; Chlamydiales; Chlamydiaceae; Chlamydia.
 RN NCBI TaxID=83558;
 RX SEQUENCE FROM N.A.
 RC STRAIN=VR1310;
 RX MEDLINE=20007584; PubMed=10539856;
 RA Christiansen G., Boesen T., Hjerno K., Dagaard L., Mygind P.,
 RA Madsen A.S., Knudsen K., Falk E., Birkegaard S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
 RT role in immunopathogenicity";
 RL Am. Heart J. 138:S491-S495(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206506; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 RL Nat. Genet. 21:385-389(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39.";

Nucleic Acids Res. 28:1397-1406(2000).
 [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=U138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shikai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CWL029 from USA";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=TW-183;
 RA Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
 Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 other Chlamydia strains based on whole genome sequence analysis";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 CC (Potential).
 CC -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
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 CC -----
 DR EMBL; AJ133034; CAB37069.1; -
 DR EMBL; AB001628; AAD18591.1; -
 DR EMBL; AB002192; AAF38163.1; -
 DR EMBL; AB002546; BAA98655.1; -
 DR EMBL; AB017158; AAP98395.1; -
 DR PIR; B72077; B72077.
 DR PIR; E86546; E86546.
 DR TIGR; CP0306; -
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR003368; Chlamydia PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF02415; Chlamydia PMP; 2.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMs; TIGR01376; POMP repeat; 6.
 DR Outer membrane; Signal; Multigene family; Complete proteome.
 KW SIGNAL
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 928 PROBABLE OUTER MEMBRANE PROTEIN PMP9.
 SQ SEQUENCE 928 AA; 98332 MW; 58910A8F04F12219 CRC64;
 Query Match 41.5%; Score 1982; DB 1; Length 928;
 Best Local Similarity 45.2%; Pred. No. 4.4e-100;
 Matches 429; Conservative 150; Mismatches 327; Indels 44; Gaps 19;
 QY 1 MKSSPFKVFSTFAIPLSM-----IATETVLDSASFQDNKGNFVSRESQEDA-GIT 53
 DB 1 MKSSLHWFLLSSSLALPLSLNFSAPAAVVEINLGPINSFSG--PGYTPPAQTNADGII 58
 QY 54 YLFKGNVTLENIPTGTATKSCFNNTKGDLTFTNGNSLLFTQVDAIVAGAAVNSVV 113
 DB 59 YNLTDGVSITN-AGSPALTATSCFKETGNLSFQGHGYQFLQNIDAG--ANCTFTNTAA 115
 QY 114 DKSTTFIGSSLSFIASPGSSITTGAVSCSGSLTKNVLSLFSKPNFSTDNCGAITA 173
 DB 116 NKLLSFGSGLYSLIQI--TNATGTGAIK-STGACISQNSYCYFGQNFSDNGGALQG 172
 QY 174 KTLSLTGTTMSALSENTSSKKGAIQTSDALITGNQGVFSFSDNTSSDSGAAIITEAS 233
 DB 173 SSISLS-LNPNLTFAKNKATQKGALYSTGIGIINNTLSASFSENATANNNGAIYTEAS 231
 QY 234 VTISNNAKVSFINKVTGASSSTTGMDSGGAICAYKTSTDTKY-TLTGQMLLFSNNTST 292
 DB 232 STISSNKAISFINNSVTATSA-----TGAIYCSSTSAKPKVLTLSNDGELNFIGNTAI 285

QY 293 TAGGAIYVKKLELAGGLTLFSRNSVNGCTAPKGGAIATIEDSGELSLSDSGSDIVFLGNT 352
 DB 286 TSGGAIYTNLVSSGGPFLFKNNNAIDTAAPLGGGAIATADSGSLSLAGGDITTEGNT 345
 QY 353 V---TSTTEGTNRSSIDLG-TSAKMTALRSAAAGRAIFYDYDPIITGSSSTTVTLVKVNETP 408
 DB 346 VYKGASSQSTTTRNSINIGNTWAKIVQLRASQGTIIFYDYDPIITTSITAAALSDALNGLPD 405
 QY 409 ADSALQYTGNIIFTGKLEKSETAAADSKNLTKLQVLTSSGGTSLSKHGVTLOQTQFTQQ 458
 DB 406 LAGNPAYQGTIIFYSGEKLSEAAEAADNLKSTIQOPLTLAGGQLSLKSGVTILVAKFSQS 465
 QY 469 ADSRLEMDVGTTLLEPADTSTINNLVINISSIDAKKAKIETKATSKNLTLSGTITLLDPT 528
 DB 466 POSTLLMDAGTILETAGDTITINNLVNDLSLTKETKATIKATQASQTVLSGLSLIVDPS 525
 QY 529 GTFYENHSLRNFSQSDILELKAS--GTVTSTAVTPDPIMGEKPHYCYQGTWGIWGTGA 586
 DB 526 GNVYEDVSNWNPQVFSCLTLTADDPANIHTDLAADPLEKNPIHMGYQGNWA-LSWQEDT 584
 QY 587 ST---TATNWTKTGYINPERIGSLVPSNNAFIDISLHYLMETANEGLOGDRAFWC 643
 DB 585 ATKSKAATLTWTGTGYNPNPERGLTAVNTLWGSFVDVRSIQOLVATKVRQSQETGICW 644
 QY 644 AGLSNPFHKDSTKTRRGRHLGGVYIGNLTCSDKILSAAFCQLFGRDRDYFVAKNOG 703
 DB 645 EGISNPFHKDSIKNGFRHISAGYVVGATTILASDNLITAAFCQLFGKDRDHFINKRA 704
 QY 704 TVYGGTLYYOHNETYISLPCKLPCSLSYVP---TEIPVLFSGNLSTYTHDNLKTKYTT 760
 DB 705 SAYAASLHLQHLATLSS-----PSLLRYLPQSESEQPVLFDAQISYISKNTMKTYYTQ 758
 QY 761 YPTVKGWGNDSFALFEGGRAP-ICLDESALFEQYMPFKLQFYVAHOEKFKEQTE-AR 818
 DB 759 APKGSSWYNDGCALEGLASSLPHLTHSGLHAYFFFIKVEASYIHQDSFKERNITLVR 818
 QY 819 EFGSSRLVNLALPIGIRFKESDCODATYNLTLYGVTVDLVRNPNDCOTTLRLTSGDSWKTF 878
 DB 819 SFDSDGLINVSVPIGITFERFSRNERASYEATVIYADVVRKNPDCOTTLALLNNTSWKTT 878
 QY 879 GTNLARQALVLRAGNHFCSNFSAFQSFELRGSSRNYNVDLGAKYQF 928
 DB 879 GTNLSRQAGIGRAGIIFYAFSPNLVTSNLSMBIRGSSRSYNADLGKGFQF 928
 RESULT 3
 PMP7_CHLPN STANDARD; PRT; 936 AA.
 AC Q92898; Q9J542; Q9Z504;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable outer membrane protein pmp7 precursor (Polymorphic membrane
 protein 7) (Outer membrane protein 12).
 GN Pmp7 OR OMP12 OR CPN0445 OR CP0308 OR CPB0462.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiaophila.
 NCBI_TaxID=83558;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39."; *Nucleic Acids Res.* 28:1397-1406(2000).
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RC MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA."; *Nucleic Acids Res.* 28:2311-2314(2000).
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TW-183;
 RA Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 RT other Chlamydia strains based on whole genome sequence analysis.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 658-936 FROM N.A.
 RC STRAIN=VR1310;
 RX MEDLINE=20007584; PubMed=10539856;
 RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
 RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
 RT role in immunopathogenicity."; *Am. Heart J.* 138:S491-S495(1999).
 RL Am. Heart J. 138:S491-S495(1999).
 CC -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 CC (Potential).
 CC -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
 CC
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 CC
 DR EMBL; AE001627; AAD18589.1; -;
 DR EMBL; AE002193; AAF38165.1; -;
 DR EMBL; AF002546; BAA98653.1; -;
 DR EMBL; AE017158; AAP98393.1; -;
 DR EMBL; AJ133034; CAB37067.1; -;
 DR PIR; B81591; B81591.
 DR PIR; C72078; C72078.
 DR PIR; C86546; C86546.
 DR PHCI-2DPAGE; Q9Z898; -;
 DR TIGR; CP0308; -;
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR003368; Chlamydia PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF02415; Chlamydia PMP; 2.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMs; TIGR01376; POMP-repeat; 6.
 DR Outer membrane; Signal; Multigene family; Complete proteome.
 KW SIGNAL
 FT SIGNAL 1 23
 FT CHAIN 24 936 PROBABLE OUTER MEMBRANE PROTEIN PMP7.
 FT CONFLICT 658 666 PTHGFRHI -> EDNIYRHN (IN REF. 5).
 FT CONFLICT 822 822 Y -> H (IN REF. 1, 4 AND 5).
 SQ SEQUENCE 936 AA; 100105 MW; 3981DB3C950AF95A CRC64;
 Query Match 41.1%; Score 1964; DB 1; Length 936;
 Best Local Similarity 43.4%; Pred. No. 4.2e-99;
 Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;
 QY 1 MKSSPFFKVFSTFAIF-PLSMIATHTVLDSS-ASFDGKNGNFSVRESQE-DAGTYLLEK 57

Db 1 MKSSVSWLFFSSSILPFFSSLSIAVAEVLTDSSNNYSYDGSNGTFTVFSTDAAGTYSLL 60
 QY 58 GNVLTENIPGCTGTAITKSCFNNTKGDITFTGNGSNLLPOTVDAGTVAGAAVNSSVVDKST 117
 Db 61 SDVSFQNALGIPLAGSCFLEAGDLTFQGNHAKLPAFINAGSSATVASTSADKNL 120
 QY 118 TFIGFSSLSFIASPGSSIT-TGKGAVSCSTGSLITKNVSLLFKNFSTDRGGAITAKTL 176
 Db 121 LFNDFSRLSIISCPSSLILSPGQCALK-SVGNLSLTGNSQIIFTCNFSSDGGVINTKNF 179
 QY 177 SLTGTTMSALPSENT--SSKKGAIQISDALTITGNQGEVFSNTSSDSGAAIFTEASV 234
 Db 180 LLSGTQSOFASFSRQAFTKGQGVYATGTTIENSPIGVFSQNLAKSGGALYSTONC 239
 QY 235 TISNNAKVSFIDNKVTGASSSTTGDMGGALCAVKTSTDTKVTLTGTGNOMLFSNNTSTA 294
 Db 240 SITDNFQVIFDGNANAWAAQA---QGALCC--TTTDKVTTLTGKNNLSFTNTALTY 292
 QY 295 GGAIYVKLELASGLTLFSRNSVNGGTAPK--GGAIADSDGELSLSADSGDIVFLGNT 352
 Db 293 GGAISGLKVSISAGGPTLFQSN-ISGSAGQGGGAINIASAGELALSATSGDITFNNQ 351
 QY 353 VTSITPGTNRSSIDLGTSAKMTALRSAGRAIYFYDPTTTCGSTTFTVTLVKVNETPADSA 412
 Db 352 VTNGSTST-RNAINIIDTAKVTSIRAATGQSIYFYDPTNPCTAASTDTNLNLADANSE 410
 QY 413 LOYTGNIIFTGKELSEEAADSKNLTKLOPVTLSGGTSLSKHGVTTLQTOAFTQOADS 472
 Db 411 IEYGAIYVSEKLSPIEKALANVTIRQPAVLARGDLVLRDGVTVFKDLTQSPGR 470
 QY 473 LEMDVGTTLPEADTS-TINNIVINISSIDGAKAKIETKATSKNLTLSGTTLLDPTGTP 531
 Db 471 ILMDDGTTLSAKEANLSLNLAVNLSSUDGTNKAALKTEAADKNLSLGTIALIDTEGSF 530
 QY 532 YENHSLRNPQSYDILELK---ASGTVTSTATVPPIMGEKEHYGQGTWGPVWGTCGST 588
 Db 531 YENHLSASTYPLLELTTAGANGTITLALSTLTLOPEPTHYGYQGNW-QLSWANATSS 589
 QY 589 -TATFNWTKTYIPNPERIGSLVPSNLWNADFIDISSLHLMETANEGLQGDRAPWCAGLS 647
 Db 590 KIGSINWTRTYGISPERKSNLPINSLWGNFIDIRSINQLIETKSSGFFERELWSGIA 649
 QY 648 NFFKDSKTKTRGFRHLSGGYVIGNLTHTCSKILSAAFCQLFGRDRDYFVAKNGQTVYG 707
 Db 650 NFFYRDSMPTRHGRHISGYALGITTATPAEDQLTFAFCQLFARDRNHTGKNHGDYTG 709
 QY 708 GTLYYQHNETYISLPEKL-----RPCSLSVPTHEIPVLESGNLSYTHDNLKTKYTY 761
 Db 710 ASLYPHHTTEGLFDIANFLWGKATRAPVWLSISQIIPUSFADAKFSYLHTDNNHKTYTDN 769
 QY 762 PTVKSGWGNDSFALEFGGRAPICLDESALFQYMPFMKLQFYAHQEGFKQGTBARBFG 821
 Db 770 SIKGSWENDAFCADLGASLPFVISVYPYLLKEVEFFVKQYIYAHQQDFERYAEGRAF 829
 QY 822 SSRLVNLALPTGIRPKESDCODATYNTLTGTVDLVRSNPDCTTLIRISGDSWTKFTGN 881
 Db 830 KSELINVEIPIGVTFRDSKSEKGYDILTMYILDAYRRNPKCOTSLIASDANMAYGTN 889
 QY 882 LARQALVLRAGNHCFNSNFEAFSOFSELRSGSSNNYNDLGAKYQF 928
 Db 890 LARQGSVRAANHFOVNPMPHMEIFGQFAFEVSSSRNNTNLGSKPCF 936
 RESULT 4
 PMP8 CHLPN
 ID PMP8 CHLPN STANDARD; PRT; 930 AA.
 AC Q9Z393; Q9RB66;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 10-OCT-2003 (Rel. 42, last annotation update)
 DE Probable outer membrane protein pmp8 precursor (Polymorphic membrane
 DE protein 8) (Outer membrane protein 11).

WP8 OR OMPL1 OR CPN0446 OR CP0307 OR CPB0463.
 Chlamydia pneumoniae (Chlamydophila pneumoniae).
 Bacteria; Chlamydiae; Chlamydiales; Chlamydiales; Chlamydiales; Chlamydiales.
 NCBI_TaxID=83558;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=VR1310;
 MEDLINE=20007584; PubMed=10539856;
 Christiansen G., Boesen T., Hjorne K., Daugaard L., Mygind P.,
 Madsen A.S., Knudsen K., Falk E., Birkelund S.;
 "Molecular biology of Chlamydia pneumoniae surface proteins and their
 role in immunopathogenesis";
 Am. Heart J. 138:S491-S495(1999).
 [2]
 SEQUENCE FROM N.A.
 STRAIN=CWL029;
 MEDLINE=99206606; PubMed=10192388;
 Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 Nat. Genet. 21:385-389(1999).
 [3]
 SEQUENCE FROM N.A.
 STRAIN=AR39;
 MEDLINE=20150255; PubMed=10684935;
 Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 Eisen J., Fraser C.M.;
 "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 pneumoniae AR39";
 Nucleic Acids Res. 28:1397-1406(2000).
 [4]
 SEQUENCE FROM N.A.
 STRAIN=J136;
 MEDLINE=20330349; PubMed=10871362;
 Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 Shiba T., Ishii K., Hattori M., Kubara S., Nakazawa T.;
 "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CWL029 from USA";
 Nucleic Acids Res. 28:2311-2314(2000).
 [5]
 SEQUENCE FROM N.A.
 STRAIN=TW-183;
 Geng M., Schumacher A., Muehlendorfer I., Bensch K.W., Schaefer K.P.,
 Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
 "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 other Chlamydia strains based on whole genome sequence analysis";
 Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 (Potential).
 -!- SIMILARITY: Belongs to the PMP outer membrane protein family.

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 or send an email to license@ebi-sib.ch).

 EMBL; AJ133034; CAB37068.1; -
 EMBL; AE001627; AAD18590.1; -
 EMBL; AE002193; AAF38164.1; -
 EMBL; AP002546; BAA98654.1; -
 EMBL; AE017158; AAP98394.1; -
 F1R; A81591; A81591.
 F1R; D72078; D72078.
 PHC1-2DPAGE; Q9Z393; -
 TIGR; CP0307; -
 InterPro; IPR006315; Autotransporter.
 InterPro; IPR005546; Autotransporter.

Db 818 BARAPDDGDLVNCSPVGRLEKISEDEKNNFEISLAYIGDVYRKNPRSTSLMWSGASW 877
 QY 876 KTFGTNTLAROALVLRAGNHFCFNSFEAFSPQSFELRGSSRNYYNDLCAKYOF 928
 Db 878 TSLCKNLARQAFASAGSHLTLSPHVELSGEAYELRGAHYNVDCGLRYSF 930

RESULT 5

PM11_CHLPPN
 ID PM11_CHLPPN STANDARD; PRT; 928 AA.
 AC 086164; Q9K299;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable outer membrane protein pmpl1 precursor (Polymorphic membrane protein 11) (Outer membrane protein 4).
 GN PM11 OR OMP4 OR CPN0449 OR CP0302 OR CPB0468.
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029/VR-1310;
 RX MEDLINE=99081766; PubMed=9864239;
 RA Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;
 RT "Identification of two novel genes encoding 97- to 99-kilodalton outer membrane proteins of Chlamydia pneumoniae";
 RL Infect. Immun. 67:375-383 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VR1310;
 RX MEDLINE=20007584; PubMed=10539856;
 RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
 RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity";
 RL Am. Heart J. 138:S491-S495 (1999).
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 RP SEQUENCE FROM N.A.
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 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
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 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39";
 RL Nucleic Acids Res. 28:1397-1406 (2000).
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 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA";
 RL Nucleic Acids Res. 28:2311-2314 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FW-183;
 RX Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Bessig A., Marre R., Melchers K.;
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with

RT other Chlamydia strains based on whole genome sequence analysis.";
 RL !- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 CC (Potential).
 CC !- SIMILARITY: Belongs to the PMP outer membrane protein family.
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 CC
 DR EMBL; AJ001311; CA04672.1; -
 DR EMBL; AJ13034; CAB37072.1; -
 DR EMBL; AE001628; AAD18593.1; -
 DR EMBL; AE002192; AAF38159.1; ALT_INIT.
 DR EMBL; AP002546; BAA98658.1; -
 DR EMBL; AE011158; AAP98399.1; -
 DR PIR; D72077; D72077.
 DR PIR; H86546; H86546.
 DR PHCI-2DPAGE; O86164; -
 DR TIGR; CP0302; -
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR InterPro; IPR000437; Prok_lipoprot.S.
 DR Pfam; PF02415; Chlamydia_PMP; 2.
 DR TIGRFAMs; TIGR01376; POMP repeat; 6.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 928 PROBABLE OUTER MEMBRANE PROTEIN PMP11.
 SQ SEQUENCE 928 AA; 98903 MW; 788BCDD62C911402 CRC64;
 Query Match 38.9%; Score 1855; DB 1; Length 928;
 Best Local Similarity 42.7%; Pred. No. 3.3e-93;
 Matches 405; Conservative 171; Mismatches 331; Indels 42; Gaps 20;
 QY 1 MKSFPKPVFTFAIPP--LSMIATETVLDSSASFDGN-KNGNFVRSQEDAGTYLPK 57
 Db 1 MKTSPVWLVSFLAFSCHLOSLANEELLSPDPSFNGNIDSGTFPKTS---ATTYSLT 56
 QY 58 GNVLTLETPGTCTAITKSCFNNTKGLFTPTGNGSLLFTQVDAGTVAGAAVNSVVDKST 117
 Db 57 GNVFYFE-PGKGTPLSDSCFKQTNDLTLFNGHSLTGFIDAGTHAGAA-STTAKNL 114
 QY 118 TPIGSSLSFTASPGSSITTKGAVSCSTGSLSTKNSVLSLPSKNSFNDNGCAITAKTUS 177
 Db 115 TFGFSLLSFDSPSTTWTGQTLG-SAGGVNLENIRKLVVAGNFSTADGGAIGASPL 173
 QY 178 LTGTTMSALFSENTSSKKGAIQTSDAITITGNQGEVSFSDNTSSDGAATFEASVTIS 237
 Db 174 LTGTSGLALFSSNNSSTKGAIAATTAGARIANNNTGYVFLSNIASTSGAIDDEGTSLIS 233
 QY 238 NNAKVSFDNKVTGASSSTTGDMSGGALCAVKTSTDTVTLTGNQMLFNNTSTTAGGA 297
 Db 234 NKKFYLF-----EGNAAKT---GGAICNTKASGPELITISNNKLLIFASNAETSGGA 284
 QY 298 IYVKKLELASGGLTLFSNSVNGGTAPKGGATAIEDSGELSDSGDITVLGNTWTST- 356
 Db 285 IHAKKALSSGGFTFLNNVSSAT-PKGGALSIDASGELSLSAETGNITFVRNLTITTG 343
 QY 357 -TPGNRNSIDLGTSAKMTALRSAGRAIYFYDPTTSGSTTVTVLVKNETPPASALQY 415
 Db 344 STDTPKRNAINIGSKGKTELRAAKNHTIFFYDPTT--SEGTSSTVLLKINNGSAGALNPY 401
 QY 416 TGNIIPTCKLSETEAADSKNLTSKLOPVTLSGGTFLSKHGVTLLQTAFTQOASRLBEM 475
 Db 402 QGTILFSGETILPADELKVADNLKSSFTQPVLSGGKLLLOKGVTLSTFSFSEAGSLGCM 461
 QY 476 DVGTTLE-PADTSTINNLVINISSIDGAKAKIETKATSKNLTLSGTTITLLDPTGFYEN 534
 Db 462 DSGTTLSTTAGSITITNLGINVDLSGLQPVSLTAKGASNKVIVSGKLNLIIDIEGNIYES 521

Db 173 VSAYSIDLAKTTAAALLDQNTSTKNGGALCSTANTTTVQNSGTVTFSSNTATDKGGIYS 232
QY 230 -----TEASVTISNNAKVSFDINKVTG-ASSSTITGDM 260
Db 233 KKKDSTLDANTGVVTFKSNTAKTGGAWSDDNLALTGNTQVLQENKTTGSAQAANNPEG 292
QY 261 SGAICAY-KTSTD-----TKVLTGNQMLLFSNNSTS 291
Db 293 CGGAICCYLATATDKGLAISQNEMSFTNTTANGGAIYATKCTLDGNTLTFFQNTA 352
QY 292 T----- 292
Db 353 TAGCGGAIYETEDFSLKSGTGVTFSTNTAKTGGAISYKGNSSLTGNLTNLLPSGNKATG 412
QY 293 ----- 292
Db 413 PNSSANQCGCGAAILSFLESASVTKGLWIBEDNENSVLSGNTATVSGAIYATKCALH 472
QY 293 ----- 292
Db 473 GNTLTTFDGNATAAGAIYETEDFTLTGSTGTVTFSTNTAKTAGALHTKNTSFTKNK 532
QY 293 ----- 292
Db 533 ALVFGSGSATATATTTTQCGCGAILCNISESDIATKSLTLTENESLSFINNTAKRSGG 592
QY 293 -----TAGAIYVKKLELASGGLTLFNSVNGGTAPKGGAI 329
Db 593 GIYAPKCVISGESINFDGNTAETSGAIYSKNLSITANGPVSTFNN--GG--KGGAI 647
QY 330 AIEDSGELSDAGSDIVFLGNVTSTTPTGNRSSIDLGTSAKMTALRGAAGRAIYFYDP 389
Db 648 YIADSGELSLAIDGDIETSGNEATGCTSTPN--SHLGGAGAKITKLAAPGHTIYFYDP 705
QY 390 IT---TGSSTTVTD-----VLKVNETPADSALQVYNTGNIIFTGEXL 426
Db 706 ITWEAPASGCTIEELVINPVKAIYVPPQPKNGPIASVPVVPVAPANPTGTITVFSGKL 765
QY 427 SETEADSNKLSKLOPVLTSGLTSLKHGVTLQATQOADSLEMDVGTLEPAPT 486
Db 766 PSODASIPANTTILNQNKLGNVVLKEGATLQVYSFTQDPDSTVFMWDAGTLETTT 825
QY 487 ST-----INNVINISIDGAKKAKIETKATSKNLTLSGTITLLDPTGTFYENHSLRNP 540
Db 826 NNTDGSIDLKNLSVNLDAIDGKEMITAVNSTSGGLKISGLDFHNNESFYDNPGLKAN 885
QY 541 QSYDILELKA-SGTVTSTVATPDPINGEKPHYGYQGTWG--PIVWGTGASTTATFNWTKT 597
Db 886 LNLPLFLDLSSTGTVNLDDFNPFPSSMAAPDYGYQGSWTLVPKV-GAGGKVTLVAEQAL 944
QY 598 GYIPNPERIGSLVPSNLWAFIDISLHYLMETANEGLQGDRAFCWAGLSNPFHKDSTKT 657
Db 945 GYTPKPELRATLVPSNLWAYNIHQEIAFAMSDAPSHPGIWTGGIYGNAPHODKQKE 1004
QY 658 RRGFRHLSGYVIGGNLHCTSKILSAAFCQLFGRDRDYFAKNQGTGYGTLTYOHNET 717
Db 1005 NAGFRILSRGYLVGSGMTTPEYTFVAFVSQLFGSKDYVSDIKQVYAGSLCAQ-SSY 1063
QY 718 YISLPCKLRPCSLSYV-----PTPIPVFSGNLGYTHTDNDLTKYTYTTPVKGSGWNSDF 773
Db 1064 VIPLHSLRRHLVKLVPPELPGETPLVLHGQVSYGRNHNMTTKLANNTQKGSMDWSHSP 1123
QY 774 ALFFGGRAPICLDSEALFQYMEFMKLOFYVAHOEGFKSQTEAREFGSRLVNLALPTG 833
Db 1124 AVEVGSLPVDLNNRYL-TSYSPYVKLVQVSVNQKGFQEVADPRIFDASHLVNVSIPMG 1182
QY 834 IRFDKESDCODATYNTLTGYTVLVRNSNPDCTTTLRISGDSWKTFTGNLARQALVLRAGN 893
Db 1183 LTFKHESAKPPSALLTLGVAVDAYDRHDPCLTSL-TNGTSWSTPATNLRSQAFPAEASG 1241
QY 894 HFCNFSNFAFSQFSFELRGSSRNYNVDLGAQYOF 928
Db 1242 HLKLLHGLDFASGSCELRSSRSRYNANCGRYSF 1276

RESULT 8

PMPI_CHLPN
ID PMPI_CHLPN STANDARD; PRT; 922 AA.
AC Q92G5; Q9KIY9; Q9Z4H9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable outer membrane protein pmpl precursor (Polymorphic membrane protein 1) (Outer membrane protein 6).
GN PMPI OR OMP6 OR CPN0005 OR CP0770 OR CPB0006.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007504; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity";
RL Am. Heart J. 138:S491-S495(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=9920606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
RL Nat. Genet. 21:385-389(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Bisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shitai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RX Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -! SUBCELLULAR LOCATION: Cell wall surface (elementary bodies) (Potential).
CC -! SIMILARITY: Belongs to the PMP outer membrane protein family.
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DR	InterPro: IPR006315; Autotransport.	
DR	InterPro: IPR005546; Autotransporter.	
DR	InterPro: IPR003368; Chlamydia PMP.	
DR	InterPro: IPR000437; Prok_lipoprot_s.	
DR	Pfam: PR03797; Autotransporter; 1.	
DR	Pfam: PR02415; Chlamydia_PMP; 1.	
DR	TIGRFAMS: TIGR01414; autotrans_bar1; 1.	
DR	TIGRFAMS: TIGR01376; POMP repeat; 6.	
KW	Outer membrane; Signal; Multigene family; Complete proteome.	
FT	SIGNAL 1 27 POTENTIAL.	
FT	CHAIN 28 1013 PROBABLE OUTER MEMBRANE PROTEIN PMPG.	
SQ	SEQUENCE 1013 AA; 107366 MW; F0327743C0A651DD CRC64;	
	Query Match 23.5%; Score 1120.5; DB 1; Length 1013;	
	Best Local Similarity 29.6%; Pred. No. 2.5e-53;	
	Matches 313; Conservative 160; Mismatches 409; Indels 177; Gaps 333;	
QY	1 MKSFPKFEVSTPAIFPLSMIA-----TETVLDSASFDGNK-NGNFVSRESQEDAGTTYL 55	
DB	1 MQTSHFHKFFLMILAYSCSLGGGYAAEIMPQIYDGETLTVSFPTVIGDSGTTVF 60	
QY	56 FKGNTVLIENTPGTGTATKSCFNNTKGDLTITGNGSNLLFQTVDAGTVAGAAVNSSVVDK 115	
DB	61 SAGELTLKLNDSIAALPLSCFGLNGSFTVLGRGHSILTFENIRTST-NGAALSDSANS 119	
QY	116 STTFIGRSSIF-----IASPGSSITTKGAVSCSTGSLSTKVNVL 157	
DB	120 LFTIEGFKELSFSCNLSLAVLPAAATNNGSQTPTTTSTPSNGTIYSKT-DLLILNNEKF 178	
QY	158 LFSKNFTDNGGAIITAKTSLTGTMTGMSALFSENTSSKKGGAIQSDALTITGNGEVSF- 216	
DB	179 SFYSNLVSGDGAIDAKSLTVQGISKLCVFQENTAQADGGACQVTSFSAMANEAPIAFI 238	
QY	217 -----SNTSSDS-----GAAIFTEASVT 235	
DB	239 ANVAVRGGGIAAVGDGGQGVSSSTSTEDPVVFSRNTAVFEDGNVARVGGIYSYGNVA 298	
QY	236 ISNNAKVSFDN-----KVTGASSSTTGM--SGGAI-C-----AKYSTDTKVT 277	
DB	299 FLANGKTLFLNVAAPVYIAAEQPTNGQASNTSDNYGDGGAIFCKNGAQAAGSNNGSVS 358	
QY	278 LTGNOMLLFSNNTSTTAGGATVYKLELASCGLTLFSRNSVNGGTPAPKGGAIATDSCGL 337	
DB	359 FDGEVVFVFSNVAAGKGALYAKLSVANGCPVOFLGNIA-----DGGAIYIGESGL 413	
QY	338 SLSADSGDIVPLGN---TVTSTTPTGN-----RSSIDLGTSAKMTALRSAAGRAIFYDP 389	
DB	414 SLSADYGDIIIFDGNLKRKTAKENAADVNGVTVSSQAISMGGCKITTLRAKAGHQILFNDP 473	
QY	390 ITTGSST-----VTDVLKVNETPADSALOYTGNIIFTGEKLSFTEAADSKNLTSLKLPV 445	
DB	474 IEMANGNNQPAQSSEPLKINDGEG-----YTGDIVFA-----NGNSTLYQNV 515	
QY	446 TLSGGLTSLKHGVTLQTAFTQQAADSRLEMDVGGTLE-----PADTS--TINNLV 493	
DB	516 TIEGRIVLRKAKLSVNSLSQTGGS-LYMAAGSTLDFVTPQPQPPAANQLITLSNLH 574	
QY	494 INISSI--DGA-----KKAKIETKATSKNLTSGTITLLDPTGTGYENHS-LR 538	
DB	575 LSLSLLANNAVTPNPTPPAQDGHPAIIGSTTAGSVTISGPIFFEDLDLDAYDRYDWLG 634	
QY	539 NPOSYDILELKASTVTSVATVPDPIMEKFP-HYGYOGTWGPVWGTCASITATP-----N 593	
DB	635 SNQKIDVLKQL-GTPQSANAPSDTLGNEMPKGYQGSW-KLAWDPNTANNGPVTLKAT 692	
QY	594 WTKTGYIENPERIGSLVNSLWNAFIDISLHYLMETANEGLQGDRAPWCAGLSNFFHKD 653	
DB	693 WTKTGYNCPERVASLVNSLWGLSILDIRSAHSAIQASVDGRSYCEGLWVSGVSNFFYHD 752	
QY	654 STKTRGRPHRLGGGVYIGNLHUTCSDKILSAFCOLFQDRDRDYFVAKNQGTVYGTLTYQ 713	
DB	753 RDALQGYRYISGGYISLGANSYFGS-SMFGLAFTVFGRSKDYVYCRSNHACISGV-- 809	

Db 265 EKGAIYTKHMLRHNGPVPWNSS-----AKLGAIAIQSGSLIIAGGSLVLFQWNS 319
Qy 353 VTSPTGPNRSSIDLTGSAKTAISAAGRAIYFVDPIITG-----SSTVTDLVKNE 406
Db 320 CHFSQDQGVRAIYLEKNALLSLEARHG-DILFDFPIQVQVWSPFSTTSALPTLRI-Q 377
Qy 407 TPADSALOYTGNIIIFTGSKLSETAADSKNITSKLLQPVLSGGTSLSKHGVTLTQTAFT 466
Db 378 TINTREA-----VIFSSNLSKEEKTEA-NLSKIQPPIELQSGCLVKDRVLSAPSL 430
Qy 467 QOADSRLMDVGTTLPEADTSTINNLVINISIDGAKKAKIETKATS-KNUTLSGTITLL 525
Db 431 QAPQALLMDVGTSLTSSDLKLTLSLPLSHSIDTENSVSQSPSLTKQIFLNS----- 486
Qy 526 DPTGTFVHSLRNPOSVDILELKASGTVTSTAVTED-PIMGEKPHYGQGTWGPVWGT 584
Db 487 -EHENFYENVELLKQDKQIDPL-----SLPKGLPHDPDQGNLSHFYQGDWN-FSWQT 540
Qy 585 G-ASTTATFNWTKTYIPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLQGDRAF-- 641
Db 541 SDQRETLVANWTANSYIIPHERQSAVANTLWNTYSDMQAVQSMINTTAAQ--GAYLFGT 598
Qy 642 WCAGLSNFF--HKDSTKTRRFRHLGGYVIGGNLHSCDKILSAFQCLFRGRDRDYFA 699
Db 599 WGSVSNLFYGHGNSGKSTDNKHSRLGLFGLSTHSLDDHSCFCLAAQGLFKGSDSFT 658
Qy 700 KNQGVYGGTLYQYHNEYIYSLPCKLRPCSLSYVPTETP--VLFSGNLSYTHTDNDLKT 756
Db 659 SADTTSY-----TAAQTQATSLIKISAQACYNESHELKT 695
Qy 757 KYTTYPTVK-GSWGNDSPALFEGGRAPICLDDESALFEQYMPFMKLFQVYAHQEGFKEQT 815
Db 696 KYRSPKEGGCAHWSAVSVEIGASIPVNSGSLFSSFSIFSKLQFGSGQDGPESRG 755
Qy 816 EAREFGSRLVNLALPIGIRDKESDQDQATNLTGLTVDLVRNPNPCTTLIRISGDSW 875
Db 756 EARAFAADSSFTNISLVPVGAIEKSKQKTRNYHFLGAYIQDLKRCVSGPVTLLKNSVTW 815
Qy 876 KFTGNLARQALVLRAGNHFCFNSNFEAFSOFSPELGRSSRNYNVDLCAKYQF 928
Db 816 DAPWNLDSRAWMLTNRALH-RFQTLVNSYMLRGQSYSLDLGTTTRF 867

RESULT 13

PMPI CHLTR
ID PMPI CHLTR STANDARD; PRT; 878 AA.
AC 084882;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp1 precursor (Polymorphic membrane protein 1).
DE protein 1).
GN PMPI OR CT874.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UM-3/Cx;
RX MEDLINE=93000809; PubMed=9784136;
RA Stephens R.S., Kaimel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
RA "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."
RT Science 282:754-759(1998).
RL -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies) (Potential).
CC -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC or send an email to license@isb-sib.ch.
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DR EMBL; AB001361; AAC68472.1; -
DR PIR; B71460; B71460.
DR InterPro; IPR003368; Chlamydia PMP.
DR Pfam; PF02415; Chlamydia PMP; 1.
DR TIGRFAMs; TIGR01376; POMP repeat; 6.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 878 PROBABLE OUTER MEMBRANE PROTEIN PMPI.
SQ SEQUENCE 878 AA; 95592 MW; DF1FA31707EE48B CRC64;

Query Match 18.1%; Score 863; DB 1; Length 878;
Best Local Similarity 30.1%; Pred. No. 1.8e-39;
Matches 260; Conservative 124; Mismatches 368; Indels 112; Gaps 23;
Qy 118 TFIGFSSLSFIASPGSSITTKGAVS-----CST-----GSLSLTKN 154
Db 74 SYCFVSKLHITDPKEALFKEKGLSIQNFRLSFTDCSSKESPSSIHQKNGQLSRNN 133
Qy 155 VSLFSPKNSFTDNGAITAKTSLTGTMTSALPSENTSSKKGAIQTSALTITGNQGEV 214
Db 134 GMSFCRNHARGSGAISADAFSLQHNYLFTAFENSSKNGGAIQ-AQTSLSNVSP 192
Qy 215 SPSNTSDSCAAIFTASVITSNNAKVSFTDNKVTGASSSTTGDMSGGAI--YKTS 271
Db 193 SFARNRDLNGAICCSNLCISGNVNPFFTGNSAT-----NGAICCSIDLNTS 242
Qy 272 TDTKVTLTGNQMLFSSNNSTTAGGAIYVKKLELASGGLTLFSRNSVNGTAPKGAIAI 331
Db 243 EKGSLSLACNETLFAASNAKEKGAIVAKHMLRYNGPVSFINNS-----AKIGGAI 297
Qy 332 EDSGELSLSADSGDIVFLGNTVTSTPGTNRSSIDLGTSAKNTALRSAGRAIYDPI 391
Db 298 QSGGSLSLAGEGSLFQNSQRTSDQGLVRNAYLEKDAILSSLEANG-DILFDFPIV 356
Qy 392 TGSSTVTVDVLKVNETPADSALQVT-----GNLIPTGKLSSETAA 432
Db 357 QESS-----KESPLPSSLOASVSPPTATASPLVIQTSANRSVIFSSERLSEK 408
Qy 433 DSKNLTSLKLPVTLSSGGLSLKHGVTLQTAFTQOADSRLMDVGTTLPEADTSTINNL 492
Db 409 PD-NLTSQLOQPIELKSGRLVKDRVLSAPSLSQDQALLIMEAGTSLKTSDDLKATL 467
Qy 493 VINISSIDGAKKAKIETKATSKNLTSLGTITLLDPTGTFYENHSLRNPSQVDILELKASG 552
Db 468 SIPLHSLDTEKSVTIH-----APNLSIQKIFLSNGSDENFYENVELLSKEQNNIPLTUS- 522
Qy 553 TVTSTAVTPDPIMGEKPHYGQGTWGPVW--GTGASTTATFNWTKTYIPNPERIGSL 609
Db 523 KEQSHLHLPDGNLS--HFGYQGDW-TFSWKDSDEGHSLIA--NWTPKNYVPHPERQSTL 577
Qy 610 VPNSLWNAFIDISSLHYLMETANEGLQGDRAF--WCAGLSNFF--HKDSTKTRRFRHLS 665
Db 578 VANTLWNTYSDMQAVQSMINTIAHG--GAYLFGTWGSVSNLIFYAHDSSGKPIDNWHRS 635
Qy 666 GGYVIGGNLHSCDKILSAACQLFRGRDRDYFAKNQGTQVYGGTLYQYHNEYIYSLPCKL 725
Db 636 LGYLFGLSTHSLDDHSCFCLAAQGLFKGSDSFTSTSTTSTIATVQAQ-----LATPL-- 688
Qy 726 RPSLSYVPTETPVLVPSGNLSYTHTDNDLTKYTTYPTVK-GSWGNDSPALFEGGRAPIC 784
Db 689 -----MKISAQACYNESIHCLKYRFSKESGWSHVSVAVGVCASIPV 735
Qy 785 LDESALFEQYMPFMKLFQVYAHQEGFKEQGTAREFGSRLVNLALPTGIRDKESDQD 844
Db 736 SNGSLFSSFSIFSKLQFGSGTQDGFESSGRIKRSFASFRNISLPMGITPEKSKQTR 795
Qy 845 ATYNLTLYGTVDLVRNPNDCITTLIRISGDSMKTFTGNLARQALVLRAGNHFCFNSNFEAF 904

Db 796 NYYIFLGYIQDKRDVESPVLKNVSWDAPMANLDSRAVMEFLTNQRAHL-RLQTL 854
QY 905 SQFSFELRGSSRNYNVDLGAQYQF 928
Db 855 LNVSVYLRGQSHSYSLDLGTTYRF 878

RESULT 14
PM21_CHLPN
ID PM21_CHLPN STANDARD; PRT: 1609 AA.
AC Q9Z6U5; Q9RB58;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable outer membrane protein pmp21 precursor (Polymorphic membrane protein 21).
GN PMP21 OR CPN0963 OR CF0897 OR CFB1000.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.,
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.",
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Winn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.",
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.",
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RA Geng M.M., Schuhmacher A., Muehlendorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
other Chlamydia strains based on whole genome sequence analysis.",
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -! SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
(potential).
CC -! SIMILARITY: Belongs to the PMP outer membrane protein family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001676; AAD19099.1; -;
DR EMBL; AE002248; AAF38684.1; -;
DR EMBL; AP002548; BAA99171.1; -;

DR EMBL; AE017160; AAP98929.1; ALT_INIT.
DR PIR; A86611; A86611.
DR PIR; H72013; H72013.
DR PHCI-2DPAGE; Q9RB58; -;
DR TIGR; CP0897; -;
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter_1.
DR Pfam; PF02415; Chlamydia_PMP_1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01376; POMP repeat; 13.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 1609 PROBABLE OUTER MEMBRANE PROTEIN PMP21.
FT CONFLICT 420 420 I -> M (IN REF. 3).
SQ SEQUENCE 1609 AA; 170865 MW; 2604C39FC4024CB CRC64;
Query Match 14.4%; Score 685.5; DB 1; Length 1609;
Best Local Similarity 24.8%; Pred. No. 1.8e-29;
Matches 254; Conservative 144; Mismatches 372; Indels 253; Gaps 36;
QY 60 VTLENIPTGTAITKSCP--NNTKGDLTFTGNLSLLFQTVDAITVAGAAVNSVVDKST 117
Db 686 VSSTDIRGGGAILAQHIFITDNT-GNLFESG-----LGGGEESSTV----- 726
QY 118 TWIGSSLSFIAPGSSITTKGAVSCSTGSLTKNVLSLLFSKNPST---DNGGAITAK 174
Db 727 -----GDLAIVGGAL--LSTNEVNVCSNQNVFSNDVTNSGDSGGAILAK 771
QY 175 TLSLTGTTMSALFSENTSSKGGAI-QTSDALITIGNQGEVFSFSDNTSSDGAIIFT-EA 232
Db 772 KVDIS-AHNSVEFVSGSGKFGGAVCALNESVNIITDNGSAVSFKNRTLGGAGVAAPQG 830
QY 233 SVTI-SNNAKVSFIDNKVTGAS-----SSTGDMSG-- 262
Db 831 SVTICGNOGNIAPKFNFFVSGENQSGGAIANSVNIQDNAGDILFVSNSTSGYGGAI 890
QY 263 --CAICAYKTSTDTKVTLTGNO-MLFNSNTSTA-----GGAIYVKKLELA--S 307
Db 891 FVGSLSVASEGSPNRTLTITGNSGDLFAKNSTQTAAASLSEKDSFGGGAITYQNLKIVKNA 950
QY 308 GGLTLFNRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNTVTSTTPGTNRSDIL 367
Db 951 GNVSFY-----GNRAPSAGVQIADGGTVCLAEFGGDLFEGNI---NFDGSFNAIHL 1001
QY 368 GTSAKMTALRSAAGRIAYFYDPTTGSST---TVTDV-----LKVNETPA-DSALQY 415
Db 1002 GNDISKIVLSAVQDKNIIIFQDAITYEENTIRGLPDKDVSPLSAPSILFNKPKQDSDAQHH 1061
QY 416 TGNITFTGKLTETEADSKNLTSLKLPVTLSSGGLSLKHGVTLTQTAFTQADSRLEM 475
Db 1062 EGTRFS-----RGVSKIPQIAAQEGTLASQNAELWLAGKQBTGSSIVL 1108
QY 476 DVGVTLEPADTSTINN-----LVINISSIDGAKKAKIETKATSKNLTLS 519
Db 1109 SAGSILRIFDSQVDSAPLPENKETVLSAGVQINNSSTPNKDKAVDTPVLADIISIT 1168
QY 520 -----GTITL-----LDPTGTFYENHS-LRNPQSYDIL 546
Db 1169 VDLSSFPVQDGTLPPLPPIIIPKGTKLHNSAIDLKIIDPTNVGVENHALLSHKDIPLI 1228
QY 547 ELKASCTVTSTAVTDPPIGKFKH-----YGYQGTW-----GPIVWGTGASIT 589
Db 1229 SILKTAGMTGTPTADASINIKIDVSLPSITPATYGTGTGVWSKSNMDEGLRVVG----- 1282
QY 590 ATFNWTKCYIENPERIGSLVNSLWNAIDISSL-----HYLMETANEGLQGDRAFWC 643
Db 1283 ----WQPTCYKLNPKQKQALVNLNLSHYTDLRALKQEIFAHTTAQRM-LDFSTNVWG 1337
QY 644 AGLSNFFHKDSTKTRGRFHLGGVYVIGNLTCSKILSAAPCOLFGR-DRDYFVAKN- 701
Db 1338 SGLGVVDCQNGEFDGFKHLHTGVALGLDTQLVEDFLIGGCGFSQFFGKTESQSYAKND 1397


```

QY 544 DILELKASGTVTSTAVTPDPEIMGEKPHYGYQGTW-----GP----- 579
Db 581 PIAPFKGA-TVTKTGF-PDGEIATPSHYGYQKWSYTWSRPLLIIPADGGFPGGSPSAN 638
QY 580 ---IVWGTGAATTAFNWTGTGYIPNPERIGSLVPNSLW-----NAFIDISLHYLMET 630
Db 639 TLYAVWNSDTLVRST-----YILDPERYGEIVNSLWISFLGNQAFSDI--LQDVLLI 689
QY 631 ANEGLOQDRAFWCAGLSNFFHKDSTKTRGFRHLSGGYVIGGNLHTCSDKILSAAFCOLF 690
Db 690 DHPGL-----SITAKALGAYVEHTPRQHEGFGSGRYGYQAALSMNYTDHTTLGLSFGQLY 745
QY 691 GRDRDYFVAKNOGTVVGGTLYYQHNETYISLPCKLRPCSLSY-----VPTETPVLFSGN 744
Db 746 GKT-----NANPYDSRCSEQWYLLSPFGQFPPIVTKSEALISWK 784
QY 745 LSYTHDNDLTKY---TTPYTVKSGWGNDSFALEFGGRAPI---CLDESALFEQY--MP 796
Db 785 AAYGYSKNHLNTYLRPDKAPKSGQGWNNNSYVYLISAHPFLNWCCLLTPLAQAWDLSG 844
QY 797 FMKLOFVYAHQBFKEQGTETGDLQRSFSRKGYNVSLPIGSSQWFTPPKK-----APSTLTIX 900
Db 845 FISAFFLGWQSKFTETGDLQRSFSRKGYNVSLPIGSSQWFTPPKK-----APSTLTIX 900
QY 851 LGYTVDLVRNPDCTTTLRISGDSWKTFTGNLQALVLRAGNHFCNFGNFAFSQFSFE 910
Db 901 LAYKPDYVRVPHNIVTVVSNQESTSISGANLERHGLFVQIHDDVVDLTEDTOAFLNYTFD 960
QY 911 LRGSRRNRYNDLGAKYQF 928
Db 961 GKNGFTNHRVSTGLKSTF 978

```

Search completed: August 10, 2004, 13:13:21
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:10:51 ; Search time 21 Seconds
(without alignments)
4250.749 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSFFKVFSTFAIFPLSM.....FELGGSRNVDLGAQYQF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78.*

2: pir1.*

3: pir2.*

4: pir3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3991	83.6	772	2	H86492
2	2058	43.1	928	2	G86546
3	2058	43.1	928	2	G81591
4	1982	41.5	928	2	E86546
5	1982	41.5	928	2	B72077
6	1965	41.2	936	2	C72078
7	1964	41.1	936	2	C86546
8	1964	41.1	936	2	B81591
9	1940	40.6	930	2	D86546
10	1940	40.6	930	2	A81591
11	1936	40.6	930	2	D72078
12	1855	38.9	928	2	H86546
13	1855	38.9	928	2	D72077
14	1855	38.9	949	2	F81591
15	1573	32.9	841	2	E72130
16	1444	30.2	1276	2	B86546
17	1444	30.2	1276	2	C81591
18	1442.5	30.2	922	2	B72131
19	1442.5	30.2	922	2	E86491
20	1441.5	30.2	922	2	F81539
21	1383.5	29.0	1407	2	B72078
22	1377.5	28.9	973	2	B86547
23	1377.5	28.9	973	2	F72076
24	1377.5	28.9	995	2	C81593
25	1246	26.1	712	2	E86492
26	1120.5	23.5	1013	2	G71460
27	1051	22.0	987	2	H81722
28	1017.5	21.3	445	2	E86493
29	916	19.2	359	2	C86493

30	911	19.1	867	2	F81721
31	863	18.1	878	2	B71460
32	821	17.2	494	2	D86493
33	792	16.6	427	2	A86493
34	768	16.1	186	2	G86492
35	685.5	14.4	1609	2	A86611
36	685.5	14.4	1609	2	H72013
37	672.5	14.1	978	2	G72076
38	670	14.0	947	2	G86557
39	667.5	14.0	978	2	B81593
40	667.5	14.0	978	2	C86547
41	666	14.0	947	2	D72067
42	666	14.0	1723	2	H86557
43	666	14.0	1723	2	E72067
44	666	14.0	1732	2	C81601
45	665.5	13.9	946	2	C86549

ALIGNMENTS

RESULT 1

H86492

Pmp_3 [imported] - Chlamydothila pneumoniae (strain J138)

C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001

C:Accession: H86492

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: H86492

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-772 <STO>

A:Cross-references: GB:BA000008; NID:g8978389; PIDN:BAA98226.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: pmp_3_2

Query Match	83.6%;	Score 3991;	DB 2;	Length 772;		
Best Local Similarity	99.9%;	Pred. No. 2.3e-208;				
Matches 771;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	157	LLFSKNFSTDNGGAI	TAKTSLTGLTGTMSALF	SENTSSKKGAIQTSDALITGNQGEVSF 216		
DB	1	MLFSKNFSTDNGGAI	TAKTSLTGLTGTMSALF	SENTSSKKGAIQTSDALITGNQGEVSF 60		
QY	217	SDNTSSDGAIAIF	TEASVTISNNAKVSFI	DNKVTGASSSTTGDMSGGAI	CAYKTSTDTKV 276	
DB	61	SDNTSSDGAIAIF	TEASVTISNNAKVSFI	DNKVTGASSSTTGDMSGGAI	CAYKTSTDTKV 120	
QY	277	TLTGNQMLF	FSNNTSTTAGGAI	VYKLELAGGGLTL	FSRNSVNGGTAPKGAIAIEDSGE 336	
DB	121	TLTGNQMLF	FSNNTSTTAGGAI	VYKLELAGGGLTL	FSRNSVNGGTAPKGAIAIEDSGE 180	
QY	337	LSLSADSGD	IVFLGNTVTTST	PGTNRSSIDLGTSAKMTAL	RSAGRAIFYDPITTSST 396	
DB	181	LSLSADSGD	IVFLGNTVTTST	PGTNRSSIDLGTSAKMTAL	RSAGRAIFYDPITTSST 240	
QY	397	TVTDVLKVN	ETPADSALQYTGNI	IIFTEKLESETEADSKNLT	SKLLOPVTLSGTTLSLKH 456	
DB	241	TVTDVLKVN	ETPADSALQYTGNI	IIFTEKLESETEADSKNLT	SKLLOPVTLSGTTLSLKH 300	
QY	457	GVTLQTA	FQQAQADSRL	EMDVGTTLEPADTST	TNNVLINISSIDGAKKAIETKATSKNL 516	
DB	301	GVTLQTA	FQQAQADSRL	EMDVGTTLEPADTST	TNNVLINISSIDGAKKAIETKATSKNL 360	
QY	517	TLSGTT	TLIDPTGTFYENH	SLRNQSYDII	LELKASGVTSTAVTPDP	IMGEKHYGQGT 576
DB	361	TLSGTT	TLIDPTGTFYENH	SLRNQSYDII	LELKASGVTSTAVTPDP	IMGEKHYGQGT 420
QY	577	WGPIV	WGTGASTTAT	ATFNWTKGTGVI	PNPERIGSIVPN	SLWNAFTDISSIHVMTANEGLQ 636

Db 421 WGVWGTGASITAFNTKTYIENPERIGSLVPSNLWNAFIDISSLHYLMETANEGLQ 480
QY 637 GDRFWCAGLSNFFHKDSTKTRGRPHLSGGVYVIGGNLHTCSDKTILSAACQLPGRDRDY 696
Db 481 GDRFWCAGLSNFFHKDSTKTRGRPHLSGGVYVIGGNLHTCSDKTILSAACQLPGRDRDY 540
QY 697 FVAKNOQTVYGGTLYYQHNETYISLPCKLRPCSLSVVPTETIPLVPSGNLSYTHTDNDLKT 756
Db 541 FVAKNOQTVYGGTLYYQHNETYISLPCKLRPCSLSVVPTETIPLVPSGNLSYTHTDNDLKT 600
QY 757 KYTTPTVKSGWGNDSFALFEGGRAPICLDESALFEQYMPFMKLQFVYAHQSGFKEQGTTE 816
Db 601 KYTTPTVKSGWGNDSFALFEGGRAPICLDESALFEQYMPFMKLQFVYAHQSGFKEQGTTE 660
QY 817 AREFGSSRLVNLALPIGRFDESKDCQDATYNLTGYVDLVRSPDCTTTLIRISGDSWK 876
Db 661 AREFGSSRLVNLALPIGRFDESKDCQDATYNLTGYVDLVRSPDCTTTLIRISGDSWK 720
QY 877 TFGTNLARQALVLRAGNHFCEFNSEAFQSFELRGSSRNYNVDLGAKYQF 928
Db 721 TFGTNLARQALVLRAGNHFCEFNSEAFQSFELRGSSRNYNVDLGAKYQF 772
RESULT 2
G86546
polymorphic outer membrane protein G family [imported] - Chlamydomophila pneumoniae (strain
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C:Accession: G86546
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: G86546
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-928 <STO>
A:Cross-references: GB:BA000008; NID:g8978821; PIDN:BAA98657.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_10
C:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G
Query Match 43.1%; Score 2058; DB 2; Length 928;
Best Local Similarity 46.7%; Pred. No. 1.2e-103;
Matches 444; Conservative 142; Mismatches 320; Indels 44; Gaps 20;
QY 1 MKSPPKFFVF-STFAIF---PLSMIATETVLSSASFDGNKN-GNFSVRESQEDAGTYYL 55
Db 1 MKSQFSLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTTPKNT--TTGIDYT 58
QY 56 FKGNTVLENIPTGTATKSCFNNTKGDLTFTGNGNSLLFQTVDACTVAGAAVNSVVDK 115
Db 59 LTGDITLQNL-GDGAALTKGCFSDTTESLSFAGKGYSLFLNKS-SAEAGAL-SVTTDK 115
QY 116 STTFICGSSLSFIASPGSITT--GKGAVSCSGSLSKTNVLSLFSKFNFTDNGGAITA 173
Db 116 NLSLTGFSLSLFLAAPSIVITPSGKAVKCG-GDLTFDNGTILPKQDYCEENGGAIST 174
QY 174 KTLSLGTMTSALFSENSS---KKGAIQTSDALITITGNQGVSVSDNTSSDGAIFT 230
Db 175 KNLSLKNSTGSIISFEGNKSATGKGAICATGTVDTNNTAPTFLFSNNIAEAGGAINS 234
QY 231 EASVTLSNNAKVFINKYTVGASSSTTGMSSGCAICAYKTSTDTKYTLTGNOMLLSNNT 290
Db 235 TGNCCTTGNTSLVFSNSVT-----ATAG--NGAL-----SGDADVTISGNQSVTSGNQ 283
QY 291 STTAGGAIYVKKLELAS--GGTLFGRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVF 348
Db 284 AVANGGAIYAKKLTLAGSGGGGSIISFNIVQGTAGNGGAISILAAGECSLSAEAGDITF 343
QY 349 LGNTVSTTTP-GNRRSSIDLGTSAKMTALSAAGRAIFYDPTTGGSTTVTDVLKNET 407

Db 344 NGNAIVATTPQTCKENSIDIGSTAKITNLRAISGHSIFPYDPTANTADSTDTLNLKA 403
QY 408 PADSAALQYTNIIFTGEKLSATEAADSKNLKSLQPVTLTSGGTLSLKHGVTLQTOAFQ 467
Db 404 DAGNSTDYSGSLVIFSGEKLSEDEAKVADNLSTLQPVTLTACNLVLRKGVLDYKGFQ 463
QY 468 QADSLEMDVGTTLBPA-DTSTINNLVINISSIDGAKAKIETKATSKNLTLSGTITLLD 526
Db 464 TAGSSVIMDAGTTLKASTEETVLTGLSIPVDSLGBGKVVIAAASAKNVALSGPILLD 523
QY 527 PTGTYENHSLNPQSYDILELKASGTVTSTIAVTPDPIMGEKFEHYGQGTWGPVW--- 582
Db 524 NQGNAYENHDLGKTQDFSVQLSALGTATTTDPAVPTVATPTHYGYQGTWG-MTWVDDT 582
QY 583 -GTGASTTATFNWTKTYIPNERIGSLVPSNLWNAFIDISSLHYLMETANEGLQDRAF 641
Db 583 ASTPKTKATLAWNTGVLNPEROGPLVPSNLWGSFSDIQAIOGVIERALSATLCSDRGF 642
QY 642 WCAGLSNFFHKDSTKTRGRPHLSGGVYVIGGNLHTCSDKILSAACQLPGRDRDYVAKN 701
Db 643 WAAGVANFLDKDKGKKYRHKSGGYATGGAATCSENLSIFAFQCLFGSKDFLVAKN 702
QY 702 QGTVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLPSGNLSYTHTDNDLTKY 758
Db 703 HTDITYAGAFYIQH---ITECSGFTGCLLDKLPGSWSHKPLVLEGQLAYSHVSNLDKTY 758
QY 759 TTYPTVKSGWGNDSFALFEGGRAPICLDESALFEQYMPFMKLQFVYAHQSGFKEQTEAR 818
Db 759 TAYPEVKGSGWGNANFMMLGASSHSYPEVLHCFDIYAPYIKLNLTVIRODSSEKGTGR 818
QY 819 EFGSRLVNLALPIGRFDESKDCQDATYNLTGYVDLVRSPDCTTTLIRISGWSKTF 878
Db 819 SFDDNSLNLSPILGIVKPEKFDSCNDFSVDLTLSYVPDLIRNDPKCTTALVISGASWET 878
QY 879 GTNLARQALVLRAGNHFCEFNSEAFQSFELRGSSRNYNVDLGAKYQF 928
Db 879 ANNLARQALQVRAGSHYAFSPMFEVLGQFVFRGSSRIYNVDLGGKQF 928
RESULT 3
G81591
polymorphic membrane protein G family CP0303 [imported] - Chlamydomophila pneumoniae (stra
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Jun-2001
C:Accession: G81591
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: G81591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-928 <REA>
A:Cross-references: GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38160.1; PID:g7189233
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0303
C:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G
Query Match 43.1%; Score 2058; DB 2; Length 928;
Best Local Similarity 46.7%; Pred. No. 1.2e-103;
Matches 444; Conservative 142; Mismatches 320; Indels 44; Gaps 20;
QY 1 MKSPPKFFVF-STFAIF---PLSMIATETVLSSASFDGNKN-GNFSVRESQEDAGTYYL 55
Db 1 MKSQFSLVLSSTLACFTSCSTVFAATAENIGPSDSFDGSTNTGTTPKNT--TTGIDYT 58
QY 56 FKGNTVLENIPTGTATKSCFNNTKGDLTFTGNGNSLLFQTVDACTVAGAAVNSVVDK 115
Db 59 LTGDITLQNL-GDGAALTKGCFSDTTESLSFAGKGYSLFLNKS-SAEAGAL-SVTTDK 115


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RESULT 5
B72077
polymorphic membrane protein G family CP0306 [imported] - Chlamydomophila pneumoniae (strain
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: B72077; B81592
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: B72077
A:Molecule type: DNA
A:Residues: 1-928 <REA>
A:Cross-references: GB:AB001628; GB:AB001363; NID:g4376730; PIDN:AA018591.1; PID:g437673
A:Experimental source: strain CWL029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: B81592
A:Molecule type: DNA
A:Residues: 1-928 <REA>
A:Cross-references: GB:AB002192; GB:AB002161; NID:g7189226; PIDN:AAF38163.1; PID:g7189223
A:Experimental source: strain AR39, HL cells
C:Genetics:
C:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G
Query Match 41.5%; Score 1982; DB 2; Length 928;
Best Local Similarity 45.2%; Pred. No. 1.5e-99;
Matches 429; Conservative 150; Mismatches 327; Indels 44; Gaps 19;
QY 1 MKSSPPKVFSTFAIFPLSM-----IATETVLDSSASFDGKNGKNGFVSRESQEDA-GTT 53
Db 1 MKSSLHWLISLSLALPLSLNFSAPAAVVEINLGTNSFG--PGTYPPAQTINADGTI 58
QY 54 YLFKNVLENIPTGTATKSCFNNTKGDITFTGNGSNLLFQTVDAAGTVAGAAVNSVV 113
Db 59 YNLTDGVISITN-AGSPALTALSCFKETTNLSFQGHGYQLIQTNDAG--ANCTPTNTAA 115
QY 114 DKSTTFIGFSSLSPTASPGSSITTKGAVSGSTGSLTKVNKSLFLPSKNSFSDNGGALTA 173
Db 116 NKLLSFGSFLSLIQT--TNATTTGAIK-STGACISQSNVSCYFPGNFNDNGGALQG 172
QY 174 KTLSTGTMTGALFSENTSKKGGAIQTSDALITGNGEVSFSDNTSSDGAALFTBAS 233
Db 173 SSISLS-LNPNLTFAKNATOKGGALYSTGGITINNTLSASFSENTAANGGALYTEAS 231
QY 234 VTISNNAKVFDINKVTGASSSTTGDMSGGAICAYKTSTDTKV-TLGNQMLLFSNNTST 292
Db 232 SPISNKAISFINNSVTATSA-----TCGAIYCSSTSAKPVLTLSDNGELNFTGNTAI 285
QY 293 TAGGAIYVKKLELASGGITLFSRNSVNGGTAPKCGAIAEBSGELSADSGDIVFLGNT 352
Db 286 TSGGAIYTDNLVLSGGTFLFNNSAIDTAAPLGAIAIADSGSLGALGDDITFEGT 345
QY 353 V---TSTTPGTRNSIDLG-TSAKMTALRSAGRAIFYDPITTTGSSSTTVTDVLKVNETP 408
Db 346 VVKGASSQTTRNSINIGNTNAKIVQLRASQNTIIFYDPITTTITAAISDALNLNGPD 405
QY 409 ADSALQYTGNIIFTGKELSETEAADSKNLTSKLQPVTLSGGTLKLGHVTLQTAFTQQ 468
Db 406 LAGNPAYQGTIYFSGEKLSEAAEADNLKSTIQOPLTAGQLSLKSGVTLVAKSFQS 465
QY 469 ADSRLMDVGTGLEPADTSTINLVINISIDGAKKATKATKATKNTLTSGLTITLLDPT 528
Db 466 PGSTLLMDAGTILEADGTITINLVNVDLSLKETKATLKATQASQVTLSGSLSLVDPS 525
QY 529 GTTFYENHSLRNQSQSDILLELKAS--GTVTSTAVTPDDPIMGKFKHYGYQGTWGPVWGTCA 586
Db 526 GNVYEDVSNWNPQVFSCLTLTADDPANIHITDLAADPLEKPNHGWYQGNWA-LSQWEDT 584
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```
QY 587 ST---TATFNWTKTGYIPNPERIGSLVPSLWNAFIDISSLHYLMETANEGLQGRAPWC 643
Db 585 ATKSAATLTWTKGYINPNERRGTIVANTLWGSFVDRSTQQLVATKVRQSQETRGITWC 644
QY 644 AGLNFFHKDSTKRRGFRHLSGGVIGNLTCSDKILSAACFQCFGRDRDYFVAKNQG 703
Db 645 EGISNFFHKDSTKINKGRFRHSAGVVGATTLASDNLITAAFCQCFGRDRDFINKNRA 704
QY 704 TVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDNLTKYTT 760
Db 705 SAYAASLHLQLATLSS-----PSLLRYLPGSESEQPVLDAQIYSIVSKNMTKTYTQ 758
QY 761 YPTVKGWGNDSFALEFCGRAP-ICLDESALFEQMPMKQFVYAHQEGKEQOTE-AR 818
Db 759 APKGESSWYNDGCALASSLPTALSHSHEGLFHAYFPFIKVEASYIHQDSFKERNITLVR 818
QY 819 EFGSSRLVNALPTGIRFDKESDQDATNLTGLTYDLVRSDPCTTTLRISGDSWKTFF 878
Db 819 SFDGDLINVSPIGITFERFSRNERASYEATVIYADVVRKNPCTTALLINNTSWKTT 878
QY 879 GTNLARQALVLRAGNHFCNSNFEAFSQSPFELRGSSRNYNVDLGAKYQF 928
Db 879 GTNLSRQAGIGKAGIFYAFSPNLEVTNLSMEIRGSSRSYNADLGKQFQF 928
RESULT 6
C72078
polymorphic outer membrane protein g family - Chlamydomophila pneumoniae (strain CWL029)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: C72078
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: C72078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <ARN>
A:Cross-references: GB:AB001627; GB:AB001363; NID:g4376721; PIDN:AA018589.1; PID:g437672
A:Experimental source: strain CWL029
C:Genetics:
C:Gene: pmp 7
C:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G
Query Match 41.2%; Score 1965; DB 2; Length 936;
Best Local Similarity 43.4%; Pred. No. 1.3e-98;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;
QY 1 MKSFPKVFSTFAIF-PLSMIATETVLDSS-ASPDGKNGKNGFVSRESQE-DAGTYYLFK 57
Db 1 MKSSVSVLFFSSSIPLFSSLSIVAAEVTLDDSSNNSYDGSNGTTFVFTTDAAGTYSLL 60
QY 58 GNVLTENIPGTGTATTKSCENNTKGLTFTGNGSNLLFQTVDAAGTVAGAAVNSVVDKST 117
Db 61 SDVSFQNALGILPIASGCFLEAGGDLTFQGNQHALKFAFINAGSAGTAVSTASADKML 120
QY 118 TFIQFSSLSFIASPGSSIT-TKGAVSGSTGSLTKVNKSLFLSKNFSFSDNGGAIKTIL 176
Db 121 LFNDFSRSLIISCPSSLISPTGQCALK-SVGNLSLTGNSQIIFTQNFSSDNGGVINTKNF 179
QY 177 SLTGTMTGALFSENT--SSKGGAIQTSDALITGNGEVSFSDNTSSDGAALFEASV 234
Db 180 LLSGTSQSPASFRNQAFTKGQGVVYATGTITIENSPIGVFSQKLAKSGGALYSTDNC 239
QY 235 TISNNAKYSFIDNKVTGASSSTTGDMSGGAICAYKTSTDTKVTLTGNQMLLFSNNTSTTA 294
Db 240 SITDNFQVIFDGSNWEAAQA-----QCGALCC--TTTDTKVTTLTGNKLSFTNNTALTY 292
QY 295 GGAIYVKKLELASGGLTLFNRNSVNGGTAPK--GGAIAEBSGELSADSGDIVFLGNT 352
Db 293 GGAISGLKVSISAGGTLTFQSN-ISGSAGQGGGAINIASAGELALSATISGDTTFNNNQ 351
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A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CP0308

C;Superfamily: Chlamydothila pneumoniae polymorphic outer membrane protein G

Query Match 41.1%; Score 1964; DB 2; Length 936;
Best Local Similarity 43.4%; Pred. No. 1.4e-98;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;

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Qy 1 MKSFPKVFSTPAIF-PLSMIAETVLDS-ASFQKNGNFVSQEQ-DAGTTLFK 57
Db 1 MKSSVSWLFFSSIFLSSLSIAAEVTLDSNNSYDGSNGTFTVFSTDAAGTYSLL 60
Qy 58 GNVLTENIPGTGTAITKCFNNTKGLTFTGNGNSLLFQTVDAAGVAGAAVNSVVDKST 117
Db 61 SDVDFQNALGIPLASCFLIEAGDLTFQGNQHALKFAFVAGSAGTVASTSAADKRL 120
Qy 118 TFIQFSSLSFIASPGSSIT-TKGAVSCSTGSLSTKVNLSLFSKNPFTDNGGAIKATYL 176
Db 121 LFNDFPSRLSIISCPSSLSPGQCALK-SVGNLSLTGNSQIIFTQNFSSDNGGVINTKNF 179
Qy 177 SLTGTTMSALPSENT--SSKGGAIQTSDALTITGNOGEVFSFNTSSDGAATFEASV 234
Db 180 LLSGTSQFASFRNQFTKGQGVVYATGTITIENSPGIVFSQMLAKSGGALYSTDNC 239
Qy 235 TISNNAKVSFIDNKVTGASSSTTGDMGGCAICAYKTISTDTKVTLTGNOMLLFSNNTSTA 294
Db 240 SITDNFQVIFDGNSAWEAQA-----QGAICC--TTTKVTLTGKNLSFTNTALTY 292
Qy 295 GGAIYVKKLELASGLTIFPSNNSVNGTAPK--GGAIIEBSGELSADSGDIVFLGNT 352
Db 293 GGAIISGLKVSISAGGPTLFQSN-ISGSSAGQGGGAINIASAGELALSATSGDITFNNQ 351
Qy 353 VTSITPGNRSIDLTGAKMTALRSAGRAIYFYDPTITGSSITVTDLKVNETPADSA 412
Db 352 VTNGSTST-RNAINIIDTAKVTSIIRATGQSIYFYDPTINPTGASTDTLNLNADANSE 410
Qy 413 LQYTGNIIFTGKLESEAAADSKNLTSKLLQPVTLSSGGLTSLKHGVTLSLQTAFTQADSR 472
Db 411 IEYGGAIYVSGEKLSPTEKAIANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQPSGR 470
Qy 473 LEMDVGTTLPEADTS-TINNLVINSSIDGAKAKIETKATSKNLTLSGTTILLDPTGTF 531
Db 471 ILMDDGTTLSAKEANLSGLAVNLSLDGTNKAAKTEAADKNTLSGTTIALIDTEGSF 530
Qy 532 YENHSLRNPOQSDILELK---ASGVTSTAVTDPDPMGEKRYGYQGTWGPVWGTGAST 588
Db 531 YENHNLKSASTYPLELTTAGANGTITLGAULTLQBPETHYQGNW-QLSWANATSS 589
Qy 589 -TATFNWTKGTYPNPERIGSLVPSNLMNAFIDISLHYLMETANEGLOGDRAPWCAGLS 647
Db 590 KIGSINWRTGTYPSPERKSNPLNSLWGNFIDIRSNLIETKSSGEPFERELWLSGIA 649
Qy 648 NFFHKDSTKTRGRPHLSGGYVIGNHLTCSKILSAARCOLFGDRDYPVAKNGQTVYG 707
Db 650 NFFYSDSMPTRGRPHISGGYALGTATTAPAEQDLTFAFCQLFARDNRHITGKNGHDTYG 709
Qy 708 GLTYQHNETYISLPCKL-----RPSLSYVPTPIPVLFSGNLSYTHDNDLKTYTTY 761
Db 710 ASLYPHHTGLEGLDIANFLWKAATRAPVWLSISQIILPSFDAKFSVLHNDNMKYTYTDN 769
Qy 762 PTVKSGWGNDSFALFGGRAPICLDESALFEQYMPMKLQFYVAHQEGKQGTAREFG 821
Db 770 SIIKGSWRNDAFCADIGSLPVISVPVLLKEVEPVKVQYIYAHQDQFERYAEGRAF 829
Qy 822 SRLVNLALPIGRPKSDCODATNLTGLYTVDLVRNPDCQTTTLRISGDSWKTFTGN 881
Db 830 KSELINVEPIGTFFERDSKSEKGTVDLTMVILDAYRNPCKQCTSLIASDANWMAIGTN 889
Qy 882 LARQALVLRAGNHFCFNSNFEAFSFPFLRGSSRNYNVDLGAQYQF 928
Db 890 LARQGSVRAANHFOVNPHEWIFGQPAFEVRSRRNYNINLGSKFCF 936
```

RESULT 9

D86546

polymorphic outer membrane protein G family [imported] - Chlamydothila pneumoniae (strain D86546)

C;Species: Chlamydothila pneumoniae, Chlamydia pneumoniae

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001

C;Accession: D86546

R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi

Nucleic Acids Res. 28, 2311-2314, 2000

A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A;Reference number: A86491; MUID:20330349; PMID:10871362

A;Accession: D86546

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-930 <STO>

A;Cross-references: GB:BA000008; NID:G8978818; PIDN:BAA98654.1; GSPDB:GN00142

A;Experimental source: strain J138

C;Genetics:

A;Gene: pmp_8

C;Superfamily: Chlamydothila pneumoniae polymorphic outer membrane protein G

Query Match 40.6%; Score 1940; DB 2; Length 930;
Best Local Similarity 43.7%; Pred. No. 2.8e-97;
Matches 416; Conservative 165; Mismatches 324; Indels 48; Gaps 17;

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Qy 1 MKSFPKVFSTPAIFPLSM-IAT---ETVLDSASFDGKNGNFVSQEQDAGTTLFK 56
Db 1 MKIPLHKLISLTVTPILLSIATYGDASLSPDSDPDGAGGSTTTPKSTADANGTNYVL 60
Qy 57 KGVNLTENIPGTGTAITKSCFNNTKGLTFTGNGNSLLFQTVDAAGVAGAAVNSVVDKLS 116
Db 61 SGNVVI-NDAGKGALTGCCCTETTGDTFTFGKGFSEFNTVDAGSNAGAAA-STADKA 118
Qy 117 TTFIGFSSLSFIASPGSSITTKGAVSCSTGSLSTKVNLSLFSKNFSTD---NGCAITA 173
Db 119 LTFIGFNSLFIAPGTTVAVSGKSTLS-SAGALNLTGNTILFQSNVSNANNGCAITA 177
Qy 174 KTLSTGTMTGALPSENTSSKGGAIQTSDALITGNOGEVFSFNTSSDGAATFEAS 233
Db 178 KTLSTSGNTSSITFTNSAKLGGAIYSSAAASISGNTGQLVFMNKGCTGGGALGFEAS 237
Qy 234 VTISNNAKVSFIDNKVTGASSSTTGDMSGGCAICAYKTISTDTKVTLTGNOMLLFSNNTST 293
Db 238 SSITQNSLSLPSGNTATDAAG-----KGGAIYCEKTEGETPILTISGKNKSLTFAENSSVT 291
Qy 294 AGGAIYVKKLELASGLTILFERNVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNTV 353
Db 292 QGGAICAHGLDLSAAGPTLFSNNRCGNTAAGKGAIAIADSGLSLSANQGDITFLGNTL 351
Qy 354 TSTT-PGNRRSIDLGTSAKMTALRSAGRAIYFYDPI---TTGSSTTVTVDLKVNETPA 409
Db 352 TSTSAPTSTRNAIYLGSSAKITNLRAAQQSIIYFYDPIASNTTGAS---DVLITNQPOS 407
Qy 410 DSALQYTGNIIFTGKLESEAAADSKNLTSLKLLQPVTLSSGGLTSLKHGVTLSLQTAFTQQA 469
Db 408 NSPLDYSGTIVFSGEKLSEADEAKADNFTSILKQPLALASGTLALXGNVELDVNGFTQTE 467
Qy 470 DSRLEMDVGTTLPEADTSTIN--NLVINISSIDGAKAKIETKATSKNLTLSGTTILLDP 527
Db 468 GSTLLMQPTKLUK-ADTEAISLTLKLVDLSEALGNKSVSIETAGANKTITLTSPLVFQDS 526
Qy 528 TGTTFENHSLRNPOQSDILELKAS-----GIVTSTAVTDPDPMGEKRYGYQGTW 578
Db 527 SGNFYESTHTINAQTPVLVFTAAASDIYTDALLTSPVQPEP-----HYGQGHWE 580
Qy 579 PIVWGTGATTTATFNWTKGTYPNPERIGSLVPSNLMNAFIDISLHYLMETANEGLOGD 638
Db 581 ATWADTSTAKSGTMTWVTGYNPNERRASVVPDLSLWSTFTDRTLQQIMTSQANSIYQ 640
Qy 639 RAFWCAGLSNPFHKDSTKTRGRPHLSGGYVIGNHLTCSKILSAARCOLFGDRDYPV 698
Db 641 RGLWASGTANPFHKDKSGTGNQAFRHKSYGYIYVGGSAEDFSENIYFSAFCQLFGKDKDLFI 700
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Qy	470	DSRLMDVGTTLLEPADSTIN--NLVIMISSIDGAKKAKIETKATSKNLTLSGTITLLDP	52
Db	468	GSTLLMQPGTKLK-ADTEAISLTKLVLDLSALEGNKSVISITAGANKITLTSLPSVQDSS	526
Qy	528	TGTEVENHSLRNPOSYDILELKAS-----GTVISTAVTPDPIMGKEHYGYOGTWG	578
Db	527	SGNFYESHTINQAFTQPLVFTATAASDIYIDALLTSPVQTPEP-----HYGYQGHWE	580
Qy	579	PIVWGTGASTTATNTWTKYIPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLQGD	638
Db	581	ATWADTSTAKSGTWTWTTGYNPNPERRASVVPDLSWASFTDRTLQQLTMTSQANSIYQ	640
Qy	639	RAFWCAGLSNPFHKDSYKTRGRPHLSGGYVIGNMLHCTSKILSAACFQIFGRDRDYFV	698
Db	641	RGLWASGTANFPHKDKSGTNOAFRHKSYGYIVGGSAAEDFSENFVAFQCLFGKDKLFI	700
Qy	699	AKNQGVVGGTFLYYOHNETHYISLPCKLRPC--SLSYVPTETPVLFSGNLSYTHTDNDLKT	756
Db	701	VENTSHYNLASLYLQHRAFGLGLP---MPSRGSITDMLKDPLIINAQLSYSTKNDMDT	757
Qy	757	KYTTYPTVKGSGWGNDSFALEFGGRAPICL-DESALFEQYMPMKLQFVYAHQEGFKQGT	815
Db	758	RYTSYPEAQQSWTNNSGALELGGSLALYLPKEAPPFGYFPFLKFOAVYSRQONFKESGA	817
Qy	816	EAREFGSRLVNLALPGTIREDKESDCODATYNLTGTYVDLVRSPDCTTTLRISGDSW	875
Db	818	EARAFDGGDLVNCISPGVIRLEKISDEBKNPFELISVIGDVYRKNPKRSRTSLMWGASW	877
Qy	876	KTFGTNLARQALVLRAGNHFCFNSFEAFSOFSELRGSSRNYNVDLGAKYOF	928
Db	878	TSLCKNLARQAFLASAGSHLTLSPHVELSGEAYELRGSAAHYNVDCGLRYSF	930

RESULT 11

D72078

polymorphic outer membrane protein g family - Chlamydoiphila pneumoniae (strain C;Species: Chlamydoiphila pneumoniae, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001

C;Accession: D72078

R;Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Gri-Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606; PMID:10192398

A;Accession: D72078

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-930 <ARN>

A;Cross-references: GB:AE001627; GB:AE001363; NID:g4376721; PIDN:AAID18590.1; P-A;Experimental source: strain CWL029

C;Genetics:

A;Gene: pmp_8

C;Superfamily: Chlamydoiphila pneumoniae polymorphic outer membrane protein G

Query Match	40.6%	Score 1936;	DB 2;	Length 930;
Best Local Similarity	43.5%	Pred. No. 4.7e-97;		
Matches	415;	Conservative 165;	Mismatches 325;	Indels 48; Gaps 17

Qy	1	MKSFPKVFSTFAIFPLSM-IAT---ETVLDSSASFQGNKGNFSPVRESQEDAGTYYLF	56
Db	1	MKPIPLKLLISLTIVTPILLISATYGDADASLSPDTSFDGAGGCTFTPKSTADANGTNVYL	60
Qy	57	KGNVTLENIPTGTAITKSCENNTKGDITFTGNGSNLLFQTVDACTVAGAAVNSVDKLS	116
Db	61	SGNYVI--NDAGKGTALTGCCCTETTGDTFTFGKYSFSPNTVDAGSNAGAAA--STTADKA	118
Qy	117	TTTGFSSLSFIASPGSSITTKGAVSCSTGSLSTKNVSLLFKNPSTD--NGCALTA	173
Db	119	LTTFGNSNLSFIAPGTTAVAGSKTSL- SAGALMTDNTGTLTFQNSVNEANNNGALIT	177
Qy	174	KTLSLTGTTMSALFSENTSSKKGAIQTSDALTTTGNQGVFSFDNTSSDSCAAIFTBAS	233
Db	178	KTLSISGNTSSINFTSNAKILGAIYSSAAAS;SGNTGOIIVFNNKCGTCGGALGPFAS	237

Qy 821 GSSRLVNLALPIGIRFDKESDCQDA--TYNLTILGYTVDLVRSPNPDCTTTTLRISGDSWKTFG 879
Dd |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
821 SIGRLNLSIPVGAKF-VQGDIGDSTYTDLSGFFSDVYRNPNQSTATVMSPDSWKIRG 879
Qy 880 TNLARQALIVLRAGHFCNSNFAPSQFSFELRGSSRNYNVDLGAKYQF 928
Dd |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
880 GNLSRQAFLRLGSGSNYYVNSCNCELFHGHYAMELRGGSSRNYNVDVGTKLRF 928

RESULT 14
F81591

Polymorphic membrane protein G family CP0302 [imported] - Chlamydomophila pneumoniae (strain C)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Jun-2001
C:Accession: F81591
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, P.A.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: F81591
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-949 <REA>
A:Cross-references: GB:AE002192; GB:AB002161; NID:g7189226; PIDN:AAF38159.1; PID:g7189226
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0302
C:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G

Query Match	38.9%	Score 1855;	DB 2;	Length 949;
Best Local Similarity	42.7%	Pred. No. 1.2e-92;		
Matches	405;	Conservative 171;	Mismatches 331;	Indels 42;
Gaps	20;			

Qy 1 MKSFPPEVFSTFAIPP--LSMIATETVLDSASFDGN-KNGNPFVSRSQEDAGTTYLPK 57
Dd :::::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
22 MKTSIPWLVSVSLAFSCHLQSLANEELLSPDDSFNGNIDSGTFTPKTS---ATTYSLT 77
Qy 58 GNTVLENI PGTGAI TKSCFNNTKGDLTETGNGSNLLFQTVDAGTVGAANSSVVVDKST 117
Dd :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
78 GDVFFYE-PKGTPLSOSCFQTTDNLTFLNGHSLTFPGIDAGTHAGAAA-STTANKNL 135
Qy 118 TFIGFSSLFIASPGSSITTKGKAVSCSTGSLSTKNVSLFSKFNSTDNGGAI TAKTLS 177
Dd :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
136 TFGSGLSLSPDSSPTVTVTGGTSL-SAGGVNLENIRKLVAAGNFSTADGGAIKGASF 194
Qy 178 LTGTMSALPSENSTSKKGAIQTSDAITITGNGEVFSFSDNTSSDGAAIPTSASVTIS 237
Dd |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
195 LTGTSGDALFSNNSSSTKGGAIATAGARIANNITGYVRFSLNIASGSAIDDEGTSILS 254
Qy 238 NNAKVSPIDNKVTGASSTTGMGGGAICAKTSDTKVTLTGQMQLFNNSTTAGCA 297
Dd |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
255 NNKFLYP-----EGNAAKTI----GGAI CNTKAGSGPELL ISNNKTLIFASNVAETSGGA 305
Qy 298 IYVKKL ELASGGLTFLFRNSYNGTAPKPGAIAIEDSGELSADS GDIVFLGNTWTST- 356
Dd :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
306 IHAKKALSSGGFTFEFLRNVS SAT-PKGAISIDASGELS SAETGNITFVRNLTITTG 364
Qy 357 -TPGTNRSSIDLGTSAKWTAIRLSAAGR AIIYPDPITTTGSSTVTVDLVKNETPADSALQY 415
Dd :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
365 STDTPKENAINIGSNGFTELR AAKNHTI PFYDPIT--SEGTSDVLKINNGSAGALNPY 422
Qy 416 TGNLI FTGK LSET EADSKNLTS KLLQPVTLSG GTLSLKHGVTLOTCAFTQQADSRLEM 475
Dd |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
423 QGITLPSGETLTAD ELKVAONLKSSFTQPVSLSGGKULLQKGVLTLESTFSQEAGSLGM 482
Qy 476 DVGTTTTLE-PADTSTINNVLVINISIDGAKKAKIETKATSKNLTLSGTTILLDPTGFYEN 534
Dd |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
483 DSGTTLSTTAGSITIINLGINVDSLGLKQPVSLTAKGASNKVI VSGKLNLDIEGNIYES 542
Qy 535 HS LRNPQSYDI ELKASGTVTS-----TAVTPDPIMGEKFHYGYOQTWGPI VMWGASTT- 589
Dd |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
543 HMFPSHDQLFSLKITTVDADVTNVDISSLIPVPAEDENSEYGFQGOANN-VNWTDTANT 601

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:14:22 ; Search time 50 Seconds
(without alignments)
5821.955 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSSFPKFVFSTFAIFPLSM.....FELGSSRNVDLGAQYF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4774	100.0	928	10	US-09-428-122-2
2	3865	81.0	746	15	US-10-312-273-19
3	2802.5	58.7	597	15	US-10-289-762-29
4	2048	42.9	928	15	US-10-312-273-95
5	1982	41.5	928	15	US-10-312-273-33
6	1965	41.2	936	9	US-09-452-380-3
7	1965	41.2	936	12	US-10-282-122A-54679
8	1965	41.2	936	14	US-10-324-129-3
9	1965	41.2	936	15	US-10-312-273-153
10	1946.5	40.8	925	9	US-09-452-380-4
11	1946.5	40.8	925	14	US-10-324-129-4
12	1940	40.6	930	15	US-10-289-762-470
13	1936	40.6	930	12	US-10-282-122A-54680
14	1936	40.6	930	15	US-10-312-273-45
15	1917.5	40.2	927	15	US-10-289-762-472

16	1915	40.1	926	10	US-09-738-269-57	Sequence 57, Appl
17	1915	40.1	926	13	US-10-023-437-57	Sequence 57, Appl
18	1856	38.9	949	15	US-10-289-762-478	Sequence 478, Appl
19	1855	38.9	928	12	US-10-282-122A-54681	Sequence 54681, A
20	1855	38.9	928	15	US-10-312-273-115	Sequence 115, Appl
21	1656.5	34.7	839	10	US-09-738-269-23	Sequence 23, Appl
22	1656.5	34.7	839	13	US-10-023-437-23	Sequence 23, Appl
23	1573	32.9	841	12	US-10-282-122A-54677	Sequence 54677, A
24	1573	32.9	841	15	US-10-312-273-139	Sequence 139, Appl
25	1572.5	32.9	841	15	US-10-289-762-474	Sequence 474, Appl
26	1442.5	30.2	922	15	US-10-312-273-41	Sequence 41, Appl
27	1437.5	30.1	922	9	US-09-886-468-19	Sequence 19, Appl
28	1437.5	30.1	922	12	US-09-889-468-19	Sequence 19, Appl
29	1417.5	29.7	922	15	US-10-289-762-15	Sequence 15, Appl
30	1383.5	29.0	1407	12	US-10-282-122A-54678	Sequence 54678, A
31	1383.5	29.0	1407	15	US-10-312-273-31	Sequence 31, Appl
32	1377.5	28.9	973	15	US-10-312-273-3	Sequence 3, Appl
33	1377.5	28.9	973	16	US-10-352-618-2	Sequence 2, Appl
34	1259	26.4	671	15	US-10-289-762-468	Sequence 468, Appl
35	1214	25.4	230	15	US-10-289-762-30	Sequence 30, Appl
36	1203.5	25.2	507	15	US-10-289-762-32	Sequence 32, Appl
37	1150	23.7	1132	15	US-10-289-762-466	Sequence 466, Appl
38	1128	23.6	1012	12	US-10-701-844-2	Sequence 2, Appl
39	1128	23.6	1012	16	US-10-766-711-2	Sequence 2, Appl
40	1126.5	23.6	1006	9	US-09-841-132-190	Sequence 190, Appl
41	1124.5	23.6	982	9	US-09-841-132-176	Sequence 176, Appl
42	1120.5	23.5	1013	16	US-10-467-534-9	Sequence 9, Appl
43	1117.5	23.4	984	12	US-10-701-844-43	Sequence 43, Appl
44	1117.5	23.4	984	16	US-10-766-711-43	Sequence 43, Appl
45	1110.5	23.3	1013	12	US-10-701-844-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-428-122-2
; Sequence 2, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Mordin et al.
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: US\$ THEREOF
; FILE REFERENCE: 19721-007-019
; CURRENT APPLICATION NUMBER: US/09/428,122
; EARLIER FILING DATE: 1999-10-27
; EARLIER FILING DATE: 1998-10-28
; EARLIER FILING DATE: 1998-10-28
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-428-122-2

Query Match	100.0%;	Score 4774;	DB 10;	Length 928;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 928;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKSSFPKFVFSTFAIFPLSMIATEVLDSSASFDGKNGNFVSRESQEDAGTYIFKGNV	60	
Db	1	MKSSFPKFVFSTFAIFPLSMIATEVLDSSASFDGKNGNFVSRESQEDAGTYIFKGNV	60	
Qy	61	TLENTPGTGTAATKSCFNNTKGLFTGTGNSLLFQTVDTAGTVAGAAVNSSVVDKSTTFI	120	
Db	61	TLENTPGTGTAATKSCFNNTKGLFTGTGNSLLFQTVDTAGTVAGAAVNSSVVDKSTTFI	120	
Qy	121	GFSSLSFIASPGSSITTKGKGVSCSTGSLTKNYSLLFSKNFSTDNGGAIKATKLSLTG	180	

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Db 121 GFSSLSFIAPSGSITTTKGAVSCSTGSLTKNVSLFNSKFNSTDNGAIIATKTLSTG 180
Qy 181 TTMSALFSENTSSKKGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNA 240
Db 181 TTMSALFSENTSSKKGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNA 240
Qy 241 KVSFIDNKVTGASSSTTGDMSGGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNA 300
Db 241 KVSFIDNKVTGASSSTTGDMSGGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNA 300
Qy 301 KKLBSAGGLTLFNRNSVNGGTAPKGGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNA 360
Db 301 KKLBSAGGLTLFNRNSVNGGTAPKGGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNA 360
Qy 361 NRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGTTLTKVLTGNQMLFSSNNTTTAGGAIYV 420
Db 361 NRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGTTLTKVLTGNQMLFSSNNTTTAGGAIYV 420
Qy 421 FTGEKLSATEAADSCKNLQPVTLSSGGLSLKHGVTLOQAFQOADSRLMDVGT 480
Db 421 FTGEKLSATEAADSCKNLQPVTLSSGGLSLKHGVTLOQAFQOADSRLMDVGT 480
Qy 481 LEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTFFYENHSLRNP 540
Db 481 LEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTFFYENHSLRNP 540
Qy 541 QSYDILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVIMVGTGASTTATFNWTKGYI 600
Db 541 QSYDILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVIMVGTGASTTATFNWTKGYI 600
Qy 601 PNPERIGSLVNSLWNAFIDISSHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRG 660
Db 601 PNPERIGSLVNSLWNAFIDISSHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRG 660
Qy 661 FPHLSGGVIVGNLHTCSDKILSAAPCOLFGRDRDYFVAKNQGTYYGGLTYQHNETYIS 720
Db 661 FPHLSGGVIVGNLHTCSDKILSAAPCOLFGRDRDYFVAKNQGTYYGGLTYQHNETYIS 720
Qy 721 LPCKLRPCSLSVPTPEIPLVPSGNLSYTHTDNDLTKYTTPTVKGSGNDSFALEFGGR 780
Db 721 LPCKLRPCSLSVPTPEIPLVPSGNLSYTHTDNDLTKYTTPTVKGSGNDSFALEFGGR 780
Qy 781 APICLDESALFEQYMPFMKQPVYAHQGEKFEQGTAREFGSSRLVNLALPIGIRFDKES 840
Db 781 APICLDESALFEQYMPFMKQPVYAHQGEKFEQGTAREFGSSRLVNLALPIGIRFDKES 840
Qy 841 DCQDATYNLTGYTVDLVRSNPDCTTTLRISGDSWKFTGTLNARQALVLRAGNHFCFNSN 900
Db 841 DCQDATYNLTGYTVDLVRSNPDCTTTLRISGDSWKFTGTLNARQALVLRAGNHFCFNSN 900
Qy 901 FFAFSQSFELRGSSRNYNVDLGAKYQF 928
Db 901 FFAFSQSFELRGSSRNYNVDLGAKYQF 928

RESULT 2
US-10-312-273-19
; Sequence 19, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
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; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqMin99, version 1.02
; SEQ ID NO 19
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-19

Query Match      81.0%; Score 3865; DB 15; Length 746;
Best Local Similarity 100.0%; Pred. No. 6,1e-281;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 MSALFSENTSSKKGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNAKV 242
Db 1 MSALFSENTSSKKGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNAKV 60
Qy 243 SFIDNKVTGASSSTTGDMSGGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNAKV 302
Db 61 SFIDNKVTGASSSTTGDMSGGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNAKV 120
Qy 303 LELASGGLTLFNRNSVNGGTAPKGGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNAKV 362
Db 121 LELASGGLTLFNRNSVNGGTAPKGGAIQTSALTTITNGQGEVSFSDNTSSDGAALFTEASVTISNNAKV 180
Qy 363 SSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGTTLTKVLTGNQMLFSSNNTTTAGGAIYVKK 422
Db 181 SSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGTTLTKVLTGNQMLFSSNNTTTAGGAIYVKK 240
Qy 423 GEKLSATEAADSCKNLQPVTLSSGGLSLKHGVTLOQAFQOADSRLMDVGT 482
Db 241 GEKLSATEAADSCKNLQPVTLSSGGLSLKHGVTLOQAFQOADSRLMDVGT 300
Qy 483 PADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTFFYENHSLRNP 542
Db 301 PADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDPTGTFFYENHSLRNP 360
Qy 543 YDILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVIMVGTGASTTATFNWTKGYI 602
Db 361 YDILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVIMVGTGASTTATFNWTKGYI 420
Qy 603 PERIGSLVNSLWNAFIDISSHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRG 662
Db 421 PERIGSLVNSLWNAFIDISSHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRG 480
Qy 663 HLSGGVIVGNLHTCSDKILSAAPCOLFGRDRDYFVAKNQGTYYGGLTYQHNETYISLP 722
Db 481 HLSGGVIVGNLHTCSDKILSAAPCOLFGRDRDYFVAKNQGTYYGGLTYQHNETYISLP 540
Qy 723 CKLRPCSLSVPTPEIPLVPSGNLSYTHTDNDLTKYTTPTVKGSGNDSFALEFGGRAP 782
Db 541 CKLRPCSLSVPTPEIPLVPSGNLSYTHTDNDLTKYTTPTVKGSGNDSFALEFGGRAP 600
Qy 783 ICLDESALFEQYMPFMKQPVYAHQGEKFEQGTAREFGSSRLVNLALPIGIRFDKESDC 842
Db 601 ICLDESALFEQYMPFMKQPVYAHQGEKFEQGTAREFGSSRLVNLALPIGIRFDKESDC 660
Qy 843 QDATYNLTGYTVDLVRSNPDCTTTLRISGDSWKFTGTLNARQALVLRAGNHFCFNSN 902
Db 661 QDATYNLTGYTVDLVRSNPDCTTTLRISGDSWKFTGTLNARQALVLRAGNHFCFNSN 720
Qy 903 FFAFSQSFELRGSSRNYNVDLGAKYQF 928
Db 721 FFAFSQSFELRGSSRNYNVDLGAKYQF 746
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?	CURRENT FILING DATE:	2002-12-20	
?	PRIOR APPLICATION NUMBER:	0016363.4	
?	PRIOR FILING DATE:	2000-07-03	
?	PRIOR APPLICATION NUMBER:	0017047.2	
?	PRIOR FILING DATE:	2000-07-11	
?	PRIOR APPLICATION NUMBER:	0017983.8	
?	PRIOR FILING DATE:	2000-07-21	
?	PRIOR APPLICATION NUMBER:	0019368.0	
?	PRIOR FILING DATE:	2000-08-07	
?	PRIOR APPLICATION NUMBER:	0020440.4	
?	PRIOR FILING DATE:	2000-08-18	
?	PRIOR APPLICATION NUMBER:	0022583.9	
?	PRIOR FILING DATE:	2000-09-14	
?	PRIOR APPLICATION NUMBER:	0027549.5	
?	PRIOR FILING DATE:	2000-11-10	
?	PRIOR APPLICATION NUMBER:	0031706.5	
?	PRIOR FILING DATE:	2000-12-22	
?	NUMBER OF SEQ ID NOS:	664	
?	SOFTWARE:	SeqWin99, version 1.02	
?	SEQ ID NO 95		
?	LENGTH:	928	
?	TYPE:	PRT	
?	ORGANISM:	Chlamydia pneumoniae	
?	US-10-312-273-95		
	Query Match	42.9%;	Score 2048; DB 15; Length 928;
	Best Local Similarity	46.5%;	Pred. No. 1.7e-144;
	Matches	442; Conservative	144; Mismatches 320; Indels 44; Gaps 20;
Qy	1	MKSFPKVF-STFAIF--PLSMIATETVLDSAGDGNKN-GNFSVRESQEDAGTYL	55
Db	1	MKSQFSLVLSLTLACFTSCSTVFAATAENIGPSDFGSGTNTGTVPKNT--TTGIDYT	58
Qy	56	FKGNVTLENIPTGTALTATKSCFNNTKGLTFTNGNSLLLPQTVDAGTVAGAAVNSVVDK	115
Db	59	LTGDITLQNL-GDSALTKGCFSDTTESFAGKGYSLFNLTKS-SAEGAAL-SVTYDK	115
Qy	116	STTFIGFSSLFASPGSSITT--GKGAVSCSTGSLTKNVSLLFKNFSTDNGGAI	173
Db	116	NLSLTGFSSLTFLAAPSIVITPSGKAVKCG-GDLTFDNNHILFKQDYCEENGAI	174
Qy	174	KTLSLTGTTMSALFSENTSS--KKGAIQTSDALITNGQGVFSNDTSSDGA	230
Db	175	KNLSLKNSTGSISEFGNKKSSATCKKGAI	234
Qy	231	EASVTISNNAKVSFIDNKVTCASSSTGDMSGAI	290
Db	235	TGNCITTGNTSLVFSNSVT---ATAG--NGGAL----	283
Qy	291	STTAGGAIYVKKLELAS--GGLTLFSRNSVNGGTAPKGAIAIEDSGELSL	348
Db	284	AVANGAIYAKUTLASGGGVFFITIVQGTAGNGAISILAGECSL	343
Qy	349	LGNTVITSTTP-GTNRSSIDLGTSAKMTALRSAGRAIFYDPDITGSS	407
Db	344	NGNAIVATTPTQTKRNSIDIGSPAKITNLRAISGHSIFFYDPITANT	403
Qy	408	PADSAIYQYTNIIFTGEKUSETAASDKNLTSLKLPVTLGGTSLKKGVT	467
Db	404	DAGNSTDYSGSIYVFSGEKLSEDAKVDNLSTLKPVTILTAGNLV	463
Qy	468	QADSRLEMDVGTLEPA-DTSTINNI	526
Db	464	TAGSSVIMDAGTILTKASTBEVLTUGUSIPVDSLGECKKVIV	523
Qy	527	PTCTFYNHSLRNPQSDYLELKA	582
Db	524	NQNAVENHDLGKTQPSFVLSALGTATTVDPAVPTATPHYGQGTG	582
Qy	583	-GTGASTATFNWTKTYIPNPERIGSLVPSNLWNAFIDISSLHYMET	641
Db	583	ASTPKTKTATLAWNTGYLPNPERQGPLVPSNLWGSFSDIQA	642


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; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-452-380-3

Query Match      41.2%; Score 1965; DB 9; Length 936;
Best Local Similarity 43.4%; Pred. No. 2.9e-138;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;

QY 1 MKSSFFKVFSTFAIF-PLSMIATEVLDSS-ASFDGKNGNPSVRESOE-DAGTYYLFK 57
Db 1 MKSSVSWLFFSSIPLFSSLSIVAAEVTLDSNNSYDGSNGTTFVSTDDAAAGTYSLL 60
QY 58 GNVTLNIPGTGTAITKSCFNNTKGLTFTGNGSNLLFQTVDAGTVAGAAVNSVVDKST 117
Db 61 SDVSVFNAGALGPIPLASGCGFLEAGGDLTFQGNHAKLFAFINAGSSAGTVASTSAADKNL 120
QY 118 TFIGFSSLSFIASPGSSIT-TGKAVSCSTGSLTKNVLSLLFSKNFSTDNGGAIKTATL 176
Db 121 LFNDFSRLLSIICPSLLSPTQCALK-SVGNLSLTGNSQIIFTQNFSSDNGGVINTKNF 179
QY 177 SLTGTTMSALFSENT--SSKKGAIQTSDALITITGQGVSPSDNTSSDGAIFTEASV 234
Db 180 LLSGTSQFASFRNQAFQTKQGGVYATGTTIENSFGIVSFQNLAKSGGALYSTDNC 239
QY 235 TISNNAKVSFIDNKVTGASSTTGDMSGGAICAYKTSTDTKVTLTGNQMLLFNNSTTTA 294
Db 240 SITDNFQVIFDGNSAWEAAQA-----QGGAICC--TTTDKVTLTGNKLSFTNTALT 292
QY 295 GGAIVYKLELAGGUTLFSRNVNGGTAPK--GGAIAEDSGELSDAGSDIVFLGNT 352
Db 293 GGAISGLKVISAGGPTLFQSN-ISGSSAGQGGGAINIASAGELALSATSGDITENNQ 351
QY 353 VSTTTEGTRSSIDLGTSAKWTALRAAGRAIYFDPITGTSSTTVTVLKVNETPADSA 412
Db 352 VINGSTST-RNAIITDITAKVTISRAATGQSIYFDPITNPGTAASDTLTNMLADANSE 410
QY 413 LQYTGNIITFGEKLSETEADSKNLAKLQPVTLGGTILSLKHGVTLOTQAFQOADS 472
Db 411 IEYGAIVFSGEKLSPTEKAIANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQPSGR 470
QY 473 LEWDGTTLEPADTS--TINNLVINISIDGAKIETKATSKNLKLSGTITLLDPTGF 531
Db 471 ILMDDGTTLSAKEANISLGLAVNLSSLDGNTKAALKTEAADKNISLSGTIALIDTEGSP 530
QY 532 YENHSLRNQSDYLELK--ASGTVTSTAVIDPDMGEKFHYGQGTWGPVWGTGAST 588
Db 531 YENHNLKSASTYPLLELTITAGANGTITLGAISLTTLQEPETHYGYQGNW-QUSWANATSS 589
QY 589 -TATFNWTKTYIPNERIGSLVPSLWNAFIDISLHVMETANEGLOQDRAFWCAGLS 647
Db 590 KIGSINWTRTYGIPSPERKSNLPLNSLWGNFIDIRSIINQLIETKSSGEPFERELWLSGIA 649
QY 648 NFPHKDSITRGRFRLHSGYVIGNHLHSCDKLSAFCQLPGRDRDVFVAKNQGVTVG 707
Db 650 NFPRDSMPTRHGRHISGAYALGITATTAPEDQLTFAFCQLFARDNRHITGNHGDITYG 709
QY 708 GTLYXOHNTYISLPCKL-----RPSLSYVTEIPVLPFSGNLSYTHTDNDLTKYTY 761
Db 710 ASLYFHHTTEGLDFIANFLMGKATRAFWLSEISQIILPSFDAKFSYLHTDNNHMTYITDN 769
QY 762 PTVKGSGNDSFALEGGRAPICLDESALFEQYMPFMKLQFVYAHQGEFKEQTEAREFG 821
Db 770 STIKGSWRNDAFCADLGASLPFVISPYLLKEVEPFVKQYIYAHQDDFERHAEGRAF 829
QY 822 SSSLVNLALPIGRPKESDQDATNLLIGYTVDLVRNPDCTTTLRISGDSWKTFTGN 881
Db 830 KSELINVERPIGVTFERDSKSEGTDLTIMYILDAYRRNPKQCTSLIASDANWMAYG 889
QY 882 LARQALVLAAGNHFCSNFEPAFSQFSFELRGSSRNVDLGAQYOF 928
Db 890 LARQGSFVRAANHFQVNPHEIFGQFAFEVRSSRNNTNLGSKFCF 936
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; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 153
; LENGTH: 936
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-10-312-273-153

Query Match
Best Local Similarity 41.2%; Score 1965; DB 15; Length 936;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;

QY 1 MKSFPKFPVSTFAIP-PLSMIATETVLDS-ASFQGNKGNFVSRESQF-DAGTYYLFK 57
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MKSSVWLFSSIFPLSSIIIVAAEVLDSNNNSYDGSNGTTFVTSTDDAAGTYSLL 60
QY 58 GNVTLNIPCTGTAITSFENNTKGLDTPFGNGSNLLFQTVDAAGTAVAGAVNSVDKST 117
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 SDVSFQAGALGIPLAGCGCELEAGGLTFQGNQHALKFAFINAGSAGTAVASTAADKNL 120
QY 118 TFGFSSLSFIAPGSSIT-TGKGAVSCSTGSLTKNVSLFLSKNPFSTDNCGAIAKTIL 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 LFNDFRSLIISCFSLLSFTGQALK-SVGNLSLTGNSQIIIFQNFSSDNGGVINTKFN 179
QY 177 SLTGTTMSALFSENT--SRKKGAIQTSALTITGNQGEVFSFSDNTSSDGAIFTEASV 234
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
180 LLSGTQFASFNRQAFQKGGVYATGTTIENSFGIVSFQNLAKGSGALYSTDC 239
QY 235 TISNNAKVSIDNKVTGASSITGDMSGGAIKAYKTSTDTKVTILTNQMLLFNNTSTTA 294
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
240 SITDNFQVIFDGNASAWAQA-----QGAIC--TTTDTKVTILTNKNLSFTNTALTY 292
QY 295 GGAIVYKLELASGGLTLFRSNVNGTAPK--GGAIAIEDSGELSLSDSGDIVFLGNT 352
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
293 GGAISGLKVISAGGPTLFQSN-ISGSSAGOGGGAINIASAGELALSATSGDITFNNQ 351
QY 353 VTSTTGTNRSSIDLGTSAKMTALRSAGAIYFYDPIITGSSTTVDVLKVNETPADSA 412
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
352 VTNGSTST-RNAIINIDTAKVTISIRAATGQSIYFYDPIITNPGTAASDTLNLNLANSE 410
QY 413 LQYTGNIIFGEXLSTEARDSKNLSKLLQPVTLSCGTLISLKHGVTLOQATQADSR 472
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
411 IEYGAIVFSGEKLSPEKAIANVSTIRQPAVLARGDLVLRDGVTVTFKDLTQPSGR 470
QY 473 LENDVGVTLEPADTS-TINNLVNISI DGAKKAKTETKATSKNLSLGTITLLDPTGT 531
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
471 ILMDGGTILSAKANLSINGLAVNLSLDGTNKAALKTEAADKNLSLGTIALIDTEGSP 530
QY 532 YENHSLRNPOSIDILEK---ASGTVTSTAVTPDPIMGEKPHYGYQGTGPIVMGTGAST 588
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
531 YENHLSKASTYPLLELTAGANGTITLGAISLTITLQEPETHYGYQGNW-QLSWANATSS 589
QY 589 -TATFNWTKGYIPNERIGSLVPSNLWNAFIDISLHYLMETANEGLQDRAFWACGLS 647
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
590 KIGSINWTRGTGYIPSPERKSNLNSLWGNFIDIRINQNIETKSGEPPERELWLSGIA 649
```

```
QY 648 NFFHKDSTTRGRFRLSGGYVIGCNLHLCSDKILSAAFCQLFGRDRDYFVAKNOGTVYG 707
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
650 NFFYRDSMPTRHGRHISGGYALGITATTPAEDQLTFAFCQLFARDNHNHITKNGHGTYG 709
QY 708 GTLYYQHNETYISLPCKL-----RPSLSYVTEIPVLPSGNLSYTHTDNDLTKYTTY 761
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
710 ASLYFHTEGLFDIANFLMGKATRAPWLSEISQIILPSLSDAKFSYHLTDNHNKTYTND 769
QY 762 PTYKSGMGNDSFALEPGGRAPICLDESALPEQYMPMKLOFVYAHQEGFKEQGTAREFG 821
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
770 SIIKSGWRNDAFCADIGASLPFVIVPYLLKEVEFPVKQYIYAHQODFYERHAEGRAF 829
QY 822 SSRVLNALPIGIRFKESDCQDATYNLTGYTVDLVRSPDCTTTLRISGDSWKTFGTN 881
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
830 KSELINVEIPIGVTFERDSKSEKTYDILTMYILDAYRNPXKCTSLIASDANWMAIGTN 889
QY 882 LARQALVLRAGNHCFNSNPEAFSOFSPELRSGSRNRYNDLGAKYQF 928
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
890 LARQGFVRAANHFQVNPHEIFGQFAFEVRSSSRNRYNTNLGSKFCF 936

RESULT 10
US-09-452-380-4
; Sequence 4, Application US/09452380
; Patent No. US20020094340A1
; GENERAL INFORMATION:
; APPLICANT: MURDIN, Andrew D.
; APPLICANT: COMEN, Raymond P.
; APPLICANT: WANG, Joe
; APPLICANT: DUNN, Pamela
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; FILE REFERENCE: 032931/0216
; CURRENT APPLICATION NUMBER: US/09/452,380
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-09-452-380-4

Query Match
Best Local Similarity 40.8%; Score 1946.5; DB 9; Length 925;
Matches 404; Conservative 177; Mismatches 319; Indels 29; Gaps 15;

QY 18 LSMIATETVLDS-ASFQGNKGNFVSRESQF-DAGTYYLFGNVLENIPGCTAITS 75
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8 LSVAAEVLDSNNNSYDGSNGTTFVTSTDAAGTYSLLSDVGFQAGALGIPLAG 67
QY 76 CFNNTXGDLTFTGNGSNLLFQTVDAAGTAVAGAVNSVVDKSTTFICFSSLSFIASPGSSI 135
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
68 CFLEAGDLTFCGNQHALKFAFINAGSAGTAVASTAADKNLLENDFRSLIISCFSL 127
QY 136 T-TGKGAVSCSTGSLTKNVSLFLSKNPFSTDNCGAIAKTILSLTGTMTSALFSENT--S 192
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
128 SPFGQCALK-SVGNLSLTGNSQIIIFQNFSSDNGGVINTKNFLSGTSQFASFRQAFT 186
QY 193 SKKGAIQTSALTITGNQGEVFSFSDNTSSDGAALFTEASVTISNNAKVSFIDNKVTA 252
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
187 GKQGVYVATGTTIENSFGIVSFQNLAKGSGALYSTDCSITDNFQVIFDGNASAWA 246
QY 253 SSSTTGDMSGGAIKAYKTSTDTKVTILTNQMLLFNNTSTTAGGAIYVVKLELASGGLTL 312
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
247 AQA-----QGAIC--TTTDTKVTILTNKNLSFTNTALTYGGLSLGKVLISAGGPTL 299
QY 313 FGRNSVNGTAPK--GGAIAIEDSGELSLSDSGDIVFLGNTVTSTTPGTRSSIDLGTS 370
```

Db 300 FQSN-19SSAGQGGGAINIASAGELALSATSQDITFNNQVNGSTST-RNAINIIDT 357
Qy 371 AKMTALRAAGRAIYFYDPIITGGSTTVDVLKVNETPADSALQVGTNIIFTEGKLSETE 430
Db 358 AKVTSIRAATGOSIVFYDPIITNPGTAASTDTLNLADANSEIEYGAIVFSGEKLSPTE 417
Qy 431 AADSKNLTSLKLOPVTLSGGTSLKHGVTLOQTAFTQOADSLEMDVGTTLLEPADTS-TI 489
Db 418 KAIANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQSPGSRILMDGGTTLISAKEANLSL 477
Qy 490 NNLVINISSIDGAKAKIETKATSKNLTSLGTTITLDDPTGTFYENHSLRNPOSYDILELK 549
Db 478 NGLAVNLSLGGTNAKALKTEAADKNISLGTIALIDTEGTFYENHSLRNPOSYDILELK 537
Qy 550 ---ASGVTSTAVTDPDPIITGKFKHYGQGTWGPVIMVGTGAST-TATFNWTKTYIPNPER 605
Db 538 TAGANGTITLGAISLTITLOEPETHYGOQNW-QLSWANATSSKIGSINWTRTYIPSPER 596
Qy 606 IGSILVPSLWAFIDISSILHYMETANEGLOQDRAPFCAGLSNPFHKDSTKTRRGRHLS 665
Db 597 KSNLPLNSLWGNFIDIRSIQIPLSFDAKFSYLHTDNHMKTYTTONSIKGSWRNDFAFADLGA 656
Qy 666 GGYVIGGNLHCTCDKILSAAPCOLFGRDRDYFAKNQGTGVTGTYLGYOHNETYISLPCKL 725
Db 657 GGYALGITTATPAEDQLTFAFCOLFARDNRHITGKHGDTYGASLYFHHTEGLFDIANFL 716
Qy 726 -----RPCSLSYVPEIPVLPSGNSLSTHTDNLKTYTTPYTKGSGWNSDFALEFGG 779
Db 717 WKGATRAPWLSEISQIPLSFDAKFSYLHTDNHMKTYTTONSIKGSWRNDFAFADLGA 776
Qy 780 RAPICLDSALPEQVMPKLOFVYAHQEGFKQGTTEAREFGSSRLVNLALDIGRFDKE 839
Db 777 SLFPFVISPVLKEVEPFVKQYIYAHQODFYERHAEGRAFNKSELINVEIPIGVTFERD 836
Qy 840 SDCQDATYNLTLGYTVDLVRSPDCTTILRISGDSWKTGFTNLARQALVLRAGNHFCFNS 899
Db 837 SKSEKGTVDLTLMYILDAYRNPCKQTSIADANMAYGTNLARQGSVRAANHFQVNP 896
Qy 900 NFEAFSQSFELGSRNRYNVDLGAQYOF 928
Db 897 HMEIFGQFAFEVRSRRNRYNVLGSKFCF 925

RESULT 11
US-10-324-129-4
; Sequence 4, Application US/10324129
; Publication No. US200301571241
; GENERAL INFORMATION:
; APPLICANT: Murdin et al.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
; FILE REFERENCE: 77813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-324-129-4

Query Match 40.8%; Score 1946.5; DB 14; Length 925;
Best Local Similarity 43.5%; Pred. No. 6.9e-137;
Matches 404; Conservative 177; Mismatches 319; Indels 29; Gaps 15;
Qy 18 LSMIAPETVLDSS-ASFDGKNGKNSVRESQF-DAGTGYLFGKNGVTLENIPGTGTAITS 75
Db 8 LSIIVAAEVLDSNNSYDGSNGTFTVFSTTDAAGTGYSLSDSVSQNAGALGIPLAGS 67

Qy 76 CFNNTKGDLTFTGNGNSLLFQTVDAQTGAGAAVNSVVDKSTTFIFGSSLSFIASPGSSI 135
Db 68 CFLEAGGDLTFQGNQHALKFAPINAGSAGTAVTSAADKKNLFLNDFRSLIISCPSLLL 127
Qy 136 T-TCKGAVSCSTGSLSLTKNVLFLSKNFSNDGGAITAKTSLTGTMTMSALFSENT--S 192
Db 128 SPTGQCALK-SVGNLSLTSNGSIITFTQNFSDNGGVINTKNFLLSGTQSFASFRNQAPT 186
Qy 193 SKKGAIQTSDALITITGNOGEVSPSDNTSSDSGAAIFTEASVTISNNAKVSFIDNKVTGA 252
Db 187 KQGGVVATGTTITENSPIVSPSONLAKSGGALYSTDNCSTIDNFQVIFDGSAMEA 246
Qy 253 SSSITGDMGGAICAYKTSTDTKVTLTQNMQLLSNNTSTTAGGAIYKVKLELASGLT 312
Db 247 AQA-----QGGAIIC--TTDDKVTLTGKNLSFTNTALTGYGGAISGLKVISAGGPTL 299
Qy 313 FSRNVNGGTAPK--GGAIAIEDSGELSDSGDIVFLGNTVTSTTPTNRRSSIDLGTS 370
Db 300 FQSN-19SSAGQGGGAINIASAGELALSATSQDITFNNQVNGSTST-RNAINIIDT 357
Qy 371 AKMTALRAAGRAIYFYDPIITGGSTTVDVLKVNETPADSALQVGTNIIFTEGKLSETE 430
Db 358 AKVTSIRAATGOSIVFYDPIITNPGTAASTDTLNLADANSEIEYGAIVFSGEKLSPTE 417
Qy 431 AADSKNLTSLKLOPVTLSGGTSLKHGVTLOQTAFTQOADSLEMDVGTTLLEPADTS-TI 489
Db 418 KAIANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQSPGSRILMDGGTTLISAKEANLSL 477
Qy 490 NNLVINISSIDGAKAKIETKATSKNLTSLGTTITLDDPTGTFYENHSLRNPOSYDILELK 549
Db 478 NGLAVNLSLGGTNAKALKTEAADKNISLGTIALIDTEGTFYENHSLRNPOSYDILELK 537
Qy 550 ---ASGVTSTAVTDPDPIITGKFKHYGQGTWGPVIMVGTGAST-TATFNWTKTYIPNPER 605
Db 538 TAGANGTITLGAISLTITLOEPETHYGOQNW-QLSWANATSSKIGSINWTRTYIPSPER 596
Qy 606 IGSILVPSLWAFIDISSILHYMETANEGLOQDRAPFCAGLSNPFHKDSTKTRRGRHLS 665
Db 597 KSNLPLNSLWGNFIDIRSIQIPLSFDAKFSYLHTDNHMKTYTTONSIKGSWRNDFAFADLGA 656
Qy 666 GGYVIGGNLHCTCDKILSAAPCOLFGRDRDYFAKNQGTGVTGTYLGYOHNETYISLPCKL 725
Db 657 GGYALGITTATPAEDQLTFAFCOLFARDNRHITGKHGDTYGASLYFHHTEGLFDIANFL 716
Qy 726 -----RPCSLSYVPEIPVLPSGNSLSTHTDNLKTYTTPYTKGSGWNSDFALEFGG 779
Db 717 WKGATRAPWLSEISQIPLSFDAKFSYLHTDNHMKTYTTONSIKGSWRNDFAFADLGA 776
Qy 780 RAPICLDSALPEQVMPKLOFVYAHQEGFKQGTTEAREFGSSRLVNLALDIGRFDKE 839
Db 777 SLFPFVISPVLKEVEPFVKQYIYAHQODFYERHAEGRAFNKSELINVEIPIGVTFERD 836
Qy 840 SDCQDATYNLTLGYTVDLVRSPDCTTILRISGDSWKTGFTNLARQALVLRAGNHFCFNS 899
Db 837 SKSEKGTVDLTLMYILDAYRNPCKQTSIADANMAYGTNLARQGSVRAANHFQVNP 896
Qy 900 NFEAFSQSFELGSRNRYNVDLGAQYOF 928
Db 897 HMEIFGQFAFEVRSRRNRYNVLGSKFCF 925

RESULT 12
US-10-289-762-470
; Sequence 470, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27

BEST AVAILABLE COPY

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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:06:40 ; Search time 58 seconds
(without alignments)
4520.760 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSFPKRVSTFAIFPLSM.....PELGRSRNVDLAKYQF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4774	100.0	928	3 AAY94327	Aay94327 Chlamydia
2	4760	99.7	928	2 AAW88421	Aaw88421 Chlamydia
3	3865	81.0	746	5 ABB90535	Abb90535 Chlamydia
4	2802.5	58.7	597	2 AAY34611	Aay34611 Chlamydia
5	2058	43.1	928	2 AAW88418	Aaw88418 Chlamydia
6	2048	42.9	928	5 ABB90573	Abb90573 Chlamydia
7	2021	42.3	928	3 AAY90237	Aay90237 Chlamydia
8	2006	42.0	918	3 AAY69369	Aay69369 Amino aci
9	2001	41.9	918	2 AAW88422	Aaw88422 Chlamydia
10	1993	41.7	914	2 AAW88429	Aaw88429 Chlamydia
11	1987.5	41.6	885	3 AAY90238	Aay90238 Mature Ch
12	1986	41.6	928	2 AAW88423	Aaw88423 Chlamydia
13	1982	41.5	928	5 ABB90542	Abb90542 Chlamydia
14	1976	41.4	928	3 AAY90239	Aay90239 Chlamydia
15	1965	41.2	936	3 AAY99842	Aay99842 Chlamydia
16	1965	41.2	936	5 ABB90602	Abb90602 Chlamydia
17	1965	41.2	936	6 ABU26755	Abu26755 Protein e
18	1946.5	40.8	925	3 AAY99843	Aay99843 Chlamydia
19	1940	40.6	930	2 AAY35052	Aay35052 Chlamydia
20	1936	40.6	930	5 ABB90548	Abb90548 Chlamydia
21	1936	40.6	930	6 ABU26756	Abu26756 Protein e
22	1930	40.4	930	3 AAY90240	Aay90240 Chlamydia
23	1927	40.4	930	2 AAW88424	Aaw88424 Chlamydia
24	1917.5	40.2	927	2 AAY35054	Aay35054 Chlamydia
25	1915	40.1	926	5 ABP56019	Abp56019 Chlamydia

26	1915	40.1	926	5 ABB98228	Abb98228 Chlamydia
27	1915	40.1	926	6 ABU6284	Abu6284 C. psitta
28	1856	38.9	949	2 AAY35060	Aay35060 Chlamydia
29	1855	38.9	928	2 AAW88417	Aaw88417 Chlamydia
30	1855	38.9	928	3 AAY90236	Aay90236 Chlamydia
31	1855	38.9	928	5 ABB90583	Abb90583 Chlamydia
32	1855	38.9	928	6 ABU26757	Abu26757 Protein e
33	1832	38.4	945	3 AAY69368	Aay69368 Amino aci
34	1811	37.9	945	2 AAW88428	Aaw88428 Chlamydia
35	1656.5	34.7	839	5 ABP56002	Abp56002 Chlamydia
36	1656.5	34.7	839	5 ABB98211	Abb98211 Chlamydia
37	1656.5	34.7	839	6 ABU6267	Abu6267 C. psitta
38	1573	32.9	841	5 ABB90595	Abb90595 Chlamydia
39	1573	32.9	841	6 ABU26753	Abu26753 Protein e
40	1572.5	32.9	643	2 AAY35056	Aay35056 Chlamydia
41	1570	32.9	841	3 AAY92818	Aay92818 C. pneumo
42	1564	32.8	841	2 AAW88420	Aaw88420 Chlamydia
43	1442.5	30.2	922	5 ABB90546	Abb90546 Chlamydia
44	1437.5	30.1	922	3 AAY95548	Aay95548 Chlamydia
45	1430.5	30.0	922	2 AAW88419	Aaw88419 Chlamydia

ALIGNMENTS

RESULT 1

AAY94327
ID AAY94327 standard; protein; 928 AA.

XX AC AAY94327;

XX AC

DT 12-SEP-2003 (revised)

DT 11-AUG-2000 (first entry)

XX DE

Chlamydia pneumoniae 98kD putative outer membrane protein.

XX KW

Chlamydia; antigen; vaccine; infection; outer membrane protein.

XX OS

Chlamydia pneumoniae.

XX XX

WO200026237-A2.

XX PD

11-MAY-2000.

XX XX

29-OCT-1999; 99WO-GB003579.

XX XX

29-OCT-1998; 98US-0106070P.

PR 01-MAR-1999; 99US-0122066P.

PR 27-OCT-1999; 99US-00428122.

XX XX

(CONN-) CONNAUGHT LAB LTD.

XX PI

Murkin AD, Oomen RP, Dunn PL;

XX PI

N-PSDB; AAA27021.

DR DR

Novel Chlamydia 98 kDa putative outer membrane protein antigen, used for vaccination and protection against Chlamydia infection.

XX XX

Claim 6; Fig 1; 93pp; English.

XX CC

The present sequence is the 98kDa putative outer membrane protein from Chlamydia pneumoniae. The genomic sequence was amplified using two PCR primers. The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence close to the 5' end of the 98kDa putative outer membrane protein coding sequence. The 3' primer contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a BglI restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame C-terminal fusion with the Histidine tag. The PCR product was cloned into a eukaryotic expression vector (pCA-Myc-His) by restricting both the vector and the PCR product with NotI and BamHI and performing a ligation

CC reaction. This expression vector was injected intramuscularly and
CC intranasally into mice, which were subsequently inoculated with Chlamydia
CC pneumoniae. The chlamydial lung titers of the immunised mice were lower
CC than those of the controls. Thus the 98kDa putative outer membrane
CC protein can be used as a vaccine to provide protection against Chlamydia
CC infections, especially Chlamydia pneumoniae infections. The present
CC polypeptide may also be administered orally to treat Chlamydia infection.
CC (Updated on 12-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 928 AA;

Query Match 100.0%; Score 4774; DB 3; Length 928;
Best Local Similarity 100.0%; Pred. No. 5.7e-307;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSFPKVFSTFAIPFLSMIATETVLDSSASFDGKNGNFSVRESQEDAGTYLFGKV 60
DB 1 MKSFPKVFSTFAIPFLSMIATETVLDSSASFDGKNGNFSVRESQEDAGTYLFGKV 60
QY 61 TLENIPGTGTAITKSCFNNTKGLFTGNGNLLFTQVDAGTVAGAAVNSSVVDKSTIFI 120
DB 61 TLENIPGTGTAITKSCFNNTKGLFTGNGNLLFTQVDAGTVAGAAVNSSVVDKSTIFI 120
QY 121 GFSSLSFIASPGSSITTKGAVSCSTGSLTKVNSLLFSKNSFTDNGGAIATAKTLISLTG 180
DB 121 GFSSLSFIASPGSSITTKGAVSCSTGSLTKVNSLLFSKNSFTDNGGAIATAKTLISLTG 180
QY 181 TTMSALFSENTSSKGGAIQTSDALITGNOGEVSFSDNTSSDGAATFEASVTISNNA 240
DB 181 TTMSALFSENTSSKGGAIQTSDALITGNOGEVSFSDNTSSDGAATFEASVTISNNA 240
QY 241 KVSFIDNKVTGASSITGDMGGAICAYKTSTDTKVLTKGNOMLLFSNNSTSTAGGAIYV 300
DB 241 KVSFIDNKVTGASSITGDMGGAICAYKTSTDTKVLTKGNOMLLFSNNSTSTAGGAIYV 300
QY 301 KXLEASGGLTLFNRNSVNGTAPKGAIAIEDSGBELSLSDSGDVIPLGNVTSTTPTGT 360
DB 301 KXLEASGGLTLFNRNSVNGTAPKGAIAIEDSGBELSLSDSGDVIPLGNVTSTTPTGT 360
QY 361 NRSSIDLGTSAKMTALRSAGRAIYFDPITGSSVTVDVLKVNTPADSALQYTGNI 420
DB 361 NRSSIDLGTSAKMTALRSAGRAIYFDPITGSSVTVDVLKVNTPADSALQYTGNI 420
QY 421 FTGEKLSEADSKNLTKLQPVTLTSGGTLTKHGVTLTQAFQQADSRLEMDVGT 480
DB 421 FTGEKLSEADSKNLTKLQPVTLTSGGTLTKHGVTLTQAFQQADSRLEMDVGT 480
QY 481 LEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTGFYENHSLRNP 540
DB 481 LEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTGFYENHSLRNP 540
QY 541 QSYDILELKASGVTSTAVTPDPIMGEKHYGQGTWGPVWGTVGASTATFNWTKTYI 600
DB 541 QSYDILELKASGVTSTAVTPDPIMGEKHYGQGTWGPVWGTVGASTATFNWTKTYI 600
QY 601 PNERIGSLVPSNLWAFIDISSILHYMETANEGLOQDRFACWAGLSNFFHKDSTKTRRG 660
DB 601 PNERIGSLVPSNLWAFIDISSILHYMETANEGLOQDRFACWAGLSNFFHKDSTKTRRG 660
QY 661 FRHLGGYVIGGNLHTCSDKILSAAPCOLFRGRDRDVFVAKNQGTGTYGTYQHNETYIS 720
DB 661 FRHLGGYVIGGNLHTCSDKILSAAPCOLFRGRDRDVFVAKNQGTGTYGTYQHNETYIS 720
QY 721 LPCKLRCSLSYVPTETPVLPSGNLSYTHTDNDLTKYTYPTVKSGWGNDSFALEFGGR 780
DB 721 LPCKLRCSLSYVPTETPVLPSGNLSYTHTDNDLTKYTYPTVKSGWGNDSFALEFGGR 780
QY 781 APICLDESALFEQWPMFKLQFYVAHQEFGKEQGTAREFGSSRLVNLALPIGIRFDKES 840
DB 781 APICLDESALFEQWPMFKLQFYVAHQEFGKEQGTAREFGSSRLVNLALPIGIRFDKES 840
QY 841 DCQDATYNLTGYTVDLVRSPDCTTTLRISGDSWKTFGTNLARQALVLRAGNHFCFNSN 900

DB 841 DCQDATYNLTGYTVDLVRSPDCTTTLRISGDSWKTFGTNLARQALVLRAGNHFCFNSN 900
QY 901 FEARSQSFELRGSSRNYNVDLGAKYQF 928
DB 901 FEARSQSFELRGSSRNYNVDLGAKYQF 928
RESULT 2
AAW88421
ID AAW88421 standard; protein; 928 AA.
XX
XX AAW88421;
AC
XX
XX 17-OCT-2003 (revised)
DT 26-APR-1999 (first entry)
DE
XX Chlamydia pneumoniae surface exposed protein Omp8.
XX
XX Omp8; outer membrane protein 8; surface exposed protein; antigen;
KW infection; diagnosis; vaccine; atherosclerosis; asthma.
XX
XX Chlamydia pneumoniae.
XX
XX WO9858953-A2.
XX
XX 30-DEC-1998.
XX
XX 19-JUN-1998; 98WO-DK0000266.
XX
XX 23-JUN-1997; 97DK-00000744.
XX
XX (BIRK/) BIRKELUND S.
XX (CHRI/) CHRISTIANSEN G.
XX
XX Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;
XX
XX WPI; 1999-105610/09.
XX
XX N-PSDB; AAX06820.
XX
XX Species-specific test for identifying mammals infected with Chlamydia
XX pneumoniae - comprises detecting antibodies specific for outer membrane
XX proteins of C. pneumoniae or nucleic acids encoding these proteins.
XX
XX Claim 7; Page 53-55; 115pp; English.
XX
XX This polypeptide comprises the novel 90.0 kDa surface exposed protein
XX Omp8 of the human respiratory pathogen Chlamydia pneumoniae. Its amino
XX acid sequence was deduced from DNA (see AAX06820) isolated from a C.
XX pneumoniae expression library. The invention provides 12 novel surface
XX exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid
XX sequences encoding them (see AAX06816-27). A new species specific test is
XX claimed that is used to identify mammals (including humans) infected with
XX Chlamydia pneumoniae. The test comprises detecting antibodies specific
XX for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
XX membrane proteins, especially by PCR. The proteins are also used in the
XX diagnosis of C. pneumoniae infection in mammals. The nucleic acids and
XX proteins can also be used in the immunization of mammals, the nucleic
XX acids being particularly useful as DNA vaccines for effecting in vivo
XX expression of antigens. The vaccines may also prevent atherosclerosis and
XX bronchial asthma, which are possibly associated with C. pneumoniae.
XX (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 928 AA;

Query Match 99.7%; Score 4760; DB 2; Length 928;
Best Local Similarity 99.7%; Pred. No. 4.8e-306;
Matches 925; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKSFPKVFSTFAIPFLSMIATETVLDSSASFDGKNGNFSVRESQEDAGTYLFGKV 60
DB 1 MKSFPKVFSTFAIPFLSMIATETVLDSSASFDGKNGNFSVRESQEDAGTYLFGKV 60
QY 61 TLENIPGTGTAITKSCFNNTKGLFTGNGNLLFTQVDAGTVAGAAVNSSVVDKSTIFI 120

Db 61 TLENIPTGTAITKSCFNNTKGLDFTTGNLSLLFQTVDAGTVAGAAVSSVWDKSTTFI 120
QY 121 GFSSLSPTASPGSSITTCGKAVSCSTGSLTKNVLFSKNFSDNCGAITAKTILSLTG 180
Db 121 GFSSLSPTASPGSSITTCGKAVSCSTGSLTKNVLFSKNFSDNCGAITAKTILSLTG 180
QY 181 TMSALFSENTSSKKGGAIOQSDALITITGNQGEVSFSDNTSSDSGAALFTEASVTISNNA 240
Db 181 TMSALFSENTSSKKGGAIOQSDALITITGNQGEVSFSDNTSSDSGAALFTEASVTISNNA 240
QY 241 KVSFIDNKVTCASSSTTGDMSGGAICAYKTDKVTILTNQMLLFSNNTTTAGGAIYV 300
Db 241 KVSFIDNKVTCASSSTTGDMSGGAICAYKTDKVTILTNQMLLFSNNTTTAGGAIYV 300
QY 301 KKLEASGLTLFNRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNVTSTTPTG 360
Db 301 KKLEASGLTLFNRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNVTSTTPTG 360
QY 361 NRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSSSTTVDVLKVNTPADSALOYTGNI 420
Db 361 NRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSSSTTVDVLKVNTPADSALOYTGNI 420
QY 421 FTGEKLSSETAADSKNLTSKLLQPVTLSSGTLKLGVTLOQTAFTQOADSRLMDVGT 480
Db 421 FTGEKLSSETAADSKNLTSKLLQPVTLSSGTLKLGVTLOQTAFTQOADSRLMDVGT 480
QY 481 LEPAADTSTINNLVINISIDGAKKAKETKATSKNLTLSTGTLTLLDPTGFYENHSLRNP 540
Db 481 LEPAADTSTINNLVINISIDGAKKAKETKATSKNLTLSTGTLTLLDPTGFYENHSLRNP 540
QY 541 QSDVILELKASGTVTSTAVTPDPIMGEKFKHYGQGTWGPVWGFGASTTATFNWTKGYI 600
Db 541 QSDVILELKASGTVTSTAVTPDPIMGEKFKHYGQGTWGPVWGFGASTTATFNWTKGYI 600
QY 601 PNERIGSLVPSNLWNAFIDISLHYMETANEGLQDRAFWCAGLSNPFHKDSTKTRRG 660
Db 601 PNERIGSLVPSNLWNAFIDISLHYMETANEGLQDRAFWCAGLSNPFHKDSTKTRRG 660
QY 661 FRHLSGGVYVGGNLTCSDKILSAFCQLFRDRDYFVAKNQGVYGGTLYYQHNETYIS 720
Db 661 FRHLSGGVYVGGNLTCSDKILSAFCQLFRDRDYFVAKNQGVYGGTLYYQHNETYIS 720
QY 721 LPCKLRPCSLSYVPTPIVPSGNLSYTHDNLTKYTYPTVKGSGNDSFALEFGGR 780
Db 721 LPCKLRPCSLSYVPTPIVPSGNLSYTHDNLTKYTYPTVKGSGNDSFALEFGGR 780
QY 781 APICLDESALFEQYMPFMKLOFYAHQEGKEQTEAREFGSSRLVNLALPIGIRFDKES 840
Db 781 APICLDESALFEQYMPFMKLOFYAHQEGKEQTEAREFGSSRLVNLALPIGIRFDKES 840
QY 841 DCQDATYNLTGLYVDLVRNPNCTTLRLISGDSWKTFFGNLAROALVLRAGNHFCFNSN 900
Db 841 DCQDATYNLTGLYVDLVRNPNCTTLRLISGDSWKTFFGNLAROALVLRAGNHFCFNSN 900
QY 901 FEAFSOFSELPGRSSRNYNVDLGAKYQF 928
Db 901 FEAFSOFSELPGRSSRNYNVDLGAKYQF 928

RESULT 3

ABB90535
ID ABB90535 standard; protein; 746 AA.

XX ABB90535;

XX ABB90535;

DT 29-AUG-2003 (revised)

DT 29-JUL-2002 (first entry)

XX Chlamydia pneumoniae cp0015 protein, SEQ ID NO:19.

XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;

XX human respiratory disease; cardiovascular disease; atherosclerosis;

coronary artery disease; carotid artery stenosis; myocardial infarction;
cerebrovascular disease; aortic aneurysm; claudication; stroke;
strain CML029.

Chlamydia pneumoniae.

WO200202606-A2.

10-JAN-2002.

03-JUL-2001; 2001WO-IB001445.

03-JUL-2000; 2000GB-00016363.

11-JUL-2000; 2000GB-00017047.

21-JUL-2000; 2000GB-00017983.

07-AUG-2000; 2000GB-00019368.

18-AUG-2000; 2000GB-00020440.

14-SEP-2000; 2000GB-00022583.

10-NOV-2000; 2000GB-00027549.

22-DEC-2000; 2000GB-00031706.

(CHIR-) CHIRON SPA.

Ratti G, Grandi G;

WPI: 2002-154726/20.

N-PSDB; ABL91193.

Novel Chlamydia pneumoniae protein useful in the manufacture of a
medicament for treatment or prevention of infection due to Chlamydia,
preferably Chlamydia pneumoniae, and for diagnostic purposes.

Claim 1; Page 49-50; 364pp; English.

Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
pneumoniae (strain CML029), and ABL91184-ABL91373 represent DNA encoding
them. The proteins are predicted to be immunogenic and may therefore be
useful in vaccine production and for diagnostic purposes. Chlamydia
pneumoniae is a common cause of respiratory disease in humans, and is
also involved in the development of cardiovascular diseases such as
atherosclerosis, coronary artery disease, carotid artery stenosis,
myocardial infarction, cerebrovascular disease, aortic aneurysm,
claudication and stroke. The proteins and nucleic acids of the invention
may be used in vaccines and pharmaceutical compositions for the
prevention or treatment of chlamydial infections, particularly Chlamydia
pneumoniae infections. The proteins may also be used in the detection of
Chlamydia pneumoniae, and the nucleic acids may be used in the detection of
DNA probe assay or blotting techniques for determining Chlamydia
pneumoniae gene expression. The present sequence represents a
specifically claimed Chlamydia pneumoniae protein of the invention.

(Updated on 29-AUG-2003 to standardise OS field)

Sequence 746 AA;

Query Match 81.0%; Score 3865; DB 5; Length 746;
Best Local Similarity 100.0%; Pred. No. 5.9e-247; Mismatches 0; Gaps 0;
Matches 746; Conservative 0; Indels 0;

QY 183 MSALFSENTSSKKGGAIOQSDALITITGNQGEVSFSDNTSSDSGAALFTEASVTISNNAKV 242

Db 1 MSALFSENTSSKKGGAIOQSDALITITGNQGEVSFSDNTSSDSGAALFTEASVTISNNAKV 60

QY 243 SFIDNKVTCASSSTTGDMSGGAICAYKTDKVTILTNQMLLFSNNTTTAGGAIYVKK 302

Db 61 SFIDNKVTCASSSTTGDMSGGAICAYKTDKVTILTNQMLLFSNNTTTAGGAIYVKK 120

QY 303 LELASGLTLFNRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNVTSTTPTGTR 362

Db 121 LELASGLTLFNRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNVTSTTPTGTR 180

QY 363 SSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSSSTTVDVLKVNTPADSALOYTGNIIFT 422

Db 181 SSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSSSTTVDVLKVNTPADSALOYTGNIIFT 240

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QY 423 GEKLETAADSKNLTSLKLPVTLGGTSLKHGVTLTQAFQQAADSRLEMDVGTILE 482
DB 241 GEKLETAADSKNLTSLKLPVTLGGTSLKHGVTLTQAFQQAADSRLEMDVGTILE 300
QY 483 PADSTINNLVINISSIDGAKKAKETKATSKNLTSLGTTITLLDPTGTFYENHSLRNPOS 542
DB 301 PADSTINNLVINISSIDGAKKAKETKATSKNLTSLGTTITLLDPTGTFYENHSLRNPOS 360
QY 543 YDILELKASGTVTSTAVTPDPIMGKPHYQGTWGPVWGTGASTTATFNWTKTYIPN 602
DB 361 YDILELKASGTVTSTAVTPDPIMGKPHYQGTWGPVWGTGASTTATFNWTKTYIPN 420
QY 603 PERIGSLVPSNLWNAFIDISSLHYLMETANEGLOGDRAFWCAGLSNFFHKDSTKTRRGFR 662
DB 421 PERIGSLVPSNLWNAFIDISSLHYLMETANEGLOGDRAFWCAGLSNFFHKDSTKTRRGFR 480
QY 663 HLSGCVYVIGGNLHTCSDKILSAAPQQLFGRDRDYFVAKNQGTVYGGTLYYQHNETYISLP 722
DB 481 HLSGCVYVIGGNLHTCSDKILSAAPQQLFGRDRDYFVAKNQGTVYGGTLYYQHNETYISLP 540
QY 723 CKLRPCSLSYVTEIPVLPFSGNLSYTHTDNDLKTKYTYPTVYKSGWGNDSFALEFGGRAP 782
DB 541 CKLRPCSLSYVTEIPVLPFSGNLSYTHTDNDLKTKYTYPTVYKSGWGNDSFALEFGGRAP 600
QY 783 ICLDESALFEQYMPFMKLQFVVAHQEGFKEQGTAREFGSSRLVNLALPIGIRFDKESDC 842
DB 601 ICLDESALFEQYMPFMKLQFVVAHQEGFKEQGTAREFGSSRLVNLALPIGIRFDKESDC 660
QY 843 QDATYNLTGYTVDLVRSNPDCSTTLRISGDSWKTFTGTNLARQALVLRAGNHFCEFSNPE 902
DB 661 QDATYNLTGYTVDLVRSNPDCSTTLRISGDSWKTFTGTNLARQALVLRAGNHFCEFSNPE 720
QY 903 AFSQSFELRGSSRNVDLGAQYQF 928
DB 721 AFSQSFELRGSSRNVDLGAQYQF 746

```

RESULT 4

AAV34611
ID AAY34611 standard; protein; 597 AA.

XX

AC AAY34611;

DT 17-OCT-2003 (revised)

DT 13-SEP-1999 (first entry)

XX

XX Chlamydia pneumoniae transmembrane protein sequence.

XX

KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope.

XX

XX Chlamydia pneumoniae.

OS

XX WO9927105-A2.

PN

XX 03-JUN-1999.

XX

XX 20-NOV-1998; 98WO-18001890.

XX

XX 21-NOV-1997; 97FR-00014673.

PR

XX 04-NOV-1998; 98US-0107078P.

XX

XX (GIST) GENSET.

PA

XX Griffais R;

PI

XX WPI; 1999-357842/30.

XX

XX Genome sequence of Chlamydia pneumoniae.

XX

XX Page 632-633; Disclosure; 1912pp; English.

PS

XX AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C.
CC pneumoniae causes respiratory disease such as pneumonia and bronchitis
CC and is thought to be a contributing factor in heart disease, sarcoidosis,
CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
CC polypeptides encoded by the open reading frames of the C. pneumoniae
CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as
CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
CC be used as immunogenic compositions, especially where the vector directs
CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
CC -OCT-2003 to standardise OS field)

XX SQ Sequence 597 AA;

Query Match 58.7%; Score 2802.5; DB 2; Length 597;
Best Local Similarity 93.8%; Pred. No. 8.7e-177;
Matches 560; Conservative 5; Mismatches 21; Indels 11; Gaps 3;

```

QY 149 LSLTKRVLLFSKNFSTONGGAIATAKTLSTGTTMSALFSENTSSKGGAIQTSALTTIT 208
DB 1 LEFDKNVLLFSKNFSTONGGAIATAKTLSTGTTMSALFSENTSSKGGAIQTSALTTIT 60
QY 209 GNOGEVPSDNTSSDGAIAFTEASVTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAY 268
DB 61 GNOGEVPSDNTSSDGAIAFTEASVTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAY 120
QY 269 KTSTDTKVTLTGNQMLLFSSNNTSTTAGGAIYVKLELASGGTLTFSRNSVWGTPAKGA 328
DB 121 KTSTDTKVTLTGNQMLLFSSNNTSTTAGGAIYVKLELASGGTLTFSRNSVWGTPAKGA 180
QY 329 IAIEDSGELSLGADSGDIVFLGNTVTSTPGTNRNSIDLTSAKMTALPSAAGRAIFYFD 388
DB 181 IAIEDSGELSLGADSGDIVFLGNTVTSTPGTNRNSIDLTSAKMTALPSAAGRAIFYFD 240
QY 389 PIITGSSSTTVTDVKNVETPADSALQYTGNIIFTGEKLETAADSKNLTSLKLPVTL 448
DB 241 PIITGSSSTTVTDVKNVETPADSALQYTGNIIFTGEKLETAADSKNLTSLKLPVTL 300
QY 449 GGTLSLKHGVTLTQAFQQAADSRLEMDVGTILEPADTSTINNLVINISSIDGAKKAKIE 508
DB 301 GGTLSLKHGVTLTQAFQQAADSRLEMDVGTILEPADTSTINNLVINISSIDGAKKAKIE 360
QY 509 TKATSKNLTSLGTTITLLDPTGTFYENHSLRNPOSYDILELKASGTVTSTAVTPDPIMGEK 568
DB 361 TKATSKNLTSLGTTITLLDPTGTFYENHSLRNPOSYDILELKASGTVTSTAVTPDPIMGEK 420
QY 569 FHYGYQGTWGPVWGTGASTTATFNWTKTYIPNPERIGSLVPSNLWNAFIDISSLHYLM 628
DB 421 FHYGYQGTWGPVWGTGASTTATFNWTKTYIPNPERIGSLVPSNLWNAFIDISSLHYLM 480
QY 629 ETANEGLOGDRAFWCAGLSNFFHKDSTKTRRGFRHLGGYVIGGNLHTCSDKILSAAPCQ 688
DB 481 ETANEGLOGDRAFWCAGLSNFFHKDSTKTRRGFRHLGGYVIGGNLHTCSDKILSAAPCQ 540
QY 689 LFGDRDRDYFAKNQGT--TVYGGTLYYQHNETYIS-----LPCKLR-PCSLSYVP 734
DB 541 LFGDRDRDYFAKNQGTLYSLRNLPAQRNLYLSLQTTALFVVLCSYRDCSLFRKP 597

```

RESULT 5

AAW88418

ID AAW88418 standard; protein; 928 AA.

XX

AC AAW88418;

XX

XX 17-OCT-2003 (revised)

DT 26-APR-1999 (first entry)

XX

XX Chlamydia pneumoniae surface exposed protein Omp5.

XX

XX Omp5; outer membrane protein 5; surface exposed protein; antigen;
KW infection; diagnosis; vaccine; atherosclerosis; asthma.

XX OS Chlamydia pneumoniae.
 XX PN WO9858953-A2.
 XX PD 30-DEC-1998.
 XX PF 19-JUN-1998; 98WO-DK000266.
 XX PR 23-JUN-1997; 97DK-00000744.
 XX PA (BIRK/) BIRKELUND S.
 XX PA (CHRI/) CHRISTIANSEN G.
 XX PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;
 XX DR WPI; 1999-105610/09.
 XX DR N-PSDB; AAX06817.
 XX PT Species-specific test for identifying mammals infected with Chlamydia
 XX PT pneumoniae - comprises detecting antibodies specific for outer membrane
 XX PT proteins of C. pneumoniae or nucleic acids encoding these proteins.
 XX PS Claim 7; Page 43-45; 115pp; English.
 XX CC This polypeptide comprises the novel 97.2 kDa surface exposed protein
 CC Omp5 of the human respiratory pathogen Chlamydia pneumoniae. Its amino
 CC acid sequence was deduced from DNA (see AAX06817) isolated from a C.
 CC pneumoniae expression library. The invention provides 12 novel surface
 CC exposed proteins, Omp4-Omp15 (see AAX06817-28), and nucleic acid
 CC sequences encoding them (see AAX06817-27). A new species specific test is
 CC claimed that is used to identify mammals (including humans) infected with
 CC Chlamydia pneumoniae. The test comprises detecting antibodies specific
 CC for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
 CC membrane proteins, especially by PCR. The proteins are also used in the
 CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids and
 CC proteins can also be used in the immunization of mammals, the nucleic
 CC acids being particularly useful as DNA vaccines for effecting in vivo
 CC expression of antigens. The vaccines may also prevent atherosclerosis and
 CC bronchial asthma, which are possibly associated with C. pneumoniae.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX SQ Sequence 928 AA;

Query Match 43.1%; Score 2058; DB 2: Length 928;
 Best Local Similarity 46.7%; Pred. No. 3e-127;
 Matches 444; Conservative 142; Mismatches 320; Indels 44; Gaps 20;

QY 1 MKSFPKVP-STFAIF---PLSMIATETVLDSASPDGNKN-GNFSVRESQBDAGTTL 55
 DB 1 MKSQFWLVLSTLACFTSCSTVPAATAENIGPDSFDGNTNGTTPKNT--TTGIDYT 58
 QY 56 FKGNVTLENIPTGTAITKSCFNNTKGDLTFTNGNSLLPQTVDAGTVAGAAVNSVVDK 115
 DB 59 LTGDITLQNL-GDSALTKGCFSDTTSLSFAGKGYSLFSLNKS-SAEGAAL-SVTYTDK 115
 QY 116 STTFIGFSSLSFLASPGSSITT--GKGVSCSTGSLTKNVLSLKNPSTONGAITA 173
 DB 116 NLSLTGFSSLTFLAAPSIVITTFSGKAVKCG-GDITFDNNNGTILPKQDYCEENGGAIST 174
 QY 174 KTLSLGTMTSALFSENSTG--KKGAIQTSDALITGNQGEVSFSDNTSSDGAIFT 230
 DB 175 KNLSLKNSTGSISEFGNKSATCKGGAICATGTVDTNNTAFLFSNNIAEAGGAINS 234
 QY 231 EASVTLSNNAKVSFIDNKVTGASSSTGDMSGGAI CAYKTSTDTKVTLTGNQMLFSNNT 290
 DB 235 TGNCITITGNTSLVFSNSVT---ATAG--NGGAL-----SGDADVTISGNQVTFSGNQ 283
 QY 291 STTAGGAIYVKKLELAS--GGLTLFERNVNGTAPKGGAIATEDSGELSLSDSGDIYF 348
 DB 284 AVANGGAIYAKKLTULASGGGGISFNNIVQGTAGNGGAIISLAAGRCSLSAEAGDITF 343
 QY 349 LGNTVITSTTP-GTNRSSIDLGTSAKMTALFSAAGRAIFYDYDPIITGSSITVTVDLVKNET 407

DB 344 NGAIVATTQTTKENSIDIGSTAKITNLRAISHSIFFDYDPIITANTAAADSTIDILNKA 403
 QY 408 PADALQYTGNIIPFTGKLSETEAAADSKNLTSLKLPVTLGGTSLKHGVTLOTQAFQ 467
 DB 404 DAGNSTDYSGSIVPSGKLSSEDAKADNLSTLTKQPVTLTAGNLVLRGVTLDTKGFTQ 463
 QY 468 QADSRLMDYGTTLLEPA-DTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLD 526
 DB 464 TAGSSVIMDAGTTLKASTEVEVTLGLSIPVDSLGEKKVWIAAASAKNVALSGPILLD 523
 QY 527 PTGTFYENHSIRNPQSYDILKASGVTSTAVTPDPIMGKPHYGGTGWPTVW---- 582
 DB 524 NQGNAYENHDLGKTQDFSVQLSALGTAITTDVPAVTVATPHYGGTGW-MTWDDT 582
 QY 583 -GTGASTTATFNWTKTYIPNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLGDRAF 641
 DB 583 ASTPKTKTATLATWNTGYPNPERQGPLVNSLWGSFSDIQAIOGVIERSAITLCSDRGF 642
 QY 642 WCAGLSNFFHKDSTKTRGRHLSGGYVIGNLTCSDKILSAAFCOLPGRDRDYFAKN 701
 DB 643 WAAGVANFLDKKGEKKRYHKSGGYAIGGAAQTCSNLSISFAFCOLFGSDKDFLAKN 702
 QY 702 QGTIVYGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHIDNDLTKY 758
 DB 703 HTDTYAGAFYQH-----ITCSCGFICLLDLKPLQSWHKPLVLEQLAYSHVSNDLTKY 758
 QY 759 TTYPTVKGWNGNSFALFEGGRAPICLDESALFEQYPMFMKLOFVYAHQBFKEQGTAR 818
 DB 759 TAYPEVKGSGWNAFNMLGASSHSPEYLHCFDTYAPYIKLNLTYIQDSFSEKGTGR 818
 QY 819 EFGSSRLNLALPIGTRFDKESCDQATYNTLTGYTVDLVRSNPDCTTILRISGDSWTF 878
 DB 819 SFDNSLNLNLPLIGWKFEKPSDCNDPSYDLTISYVFDLIRNDPKCTTALVIGASWET 878
 QY 879 GTNLARQALVLRAGNHFICNSFEATSPQSFELRGSRNVNVDLGAQYQF 928
 DB 879 ANNARQALQVRAGSHYAFSPMEVLFQGFVFEVGRSSRIYNVDLGGKFQF 928

RESULT 6
 ABB90573
 ID ABB90573 standard; protein; 928 AA.
 XX AC ABB90573;
 XX DT 29-AUG-2003 (revised)
 XX DT 29-JUL-2002 (first entry)
 XX DE Chlamydia pneumoniae cp0010 protein, SEQ ID NO:95.
 XX KW Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CWL029.
 XX OS Chlamydia pneumoniae.
 XX FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= Signal peptide
 FT 26..928
 FT Protein /note= "Mature protein"
 XX WO200202606-A2.
 XX 10-JAN-2002.
 XX 03-JUL-2001; 2001WO-IB001445.
 XX PF 03-JUL-2000; 2000GB-00016363.
 XX PR 11-JUL-2000; 2000GB-00017047.

PR 21-JUL-2000; 2000GB-00017983.
PR 07-AUG-2000; 2000GB-00019368.
PR 18-AUG-2000; 2000GB-00020440.
PR 14-SEP-2000; 2000GB-00022583.
PR 10-NOV-2000; 2000GB-00027549.
PR 22-DEC-2000; 2000GB-00031706.
XX (CHIR-) CHIRON SPA.
XX
XX Ratti G, Grandi G;
XX WPI; 2002-154726/20.
DR N-PSDB; ABL91231.
XX
XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
XX
XX Claim 1; Page 87-88; 364pp; English.
XX
XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC them. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as
CC atherosclerosis, coronary artery disease, carotid artery stenosis,
CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC claudication and stroke. The proteins and nucleic acids of the invention
CC may be used in vaccines and pharmaceutical compositions for the
CC prevention or treatment of chlamydial infections, particularly Chlamydia
CC pneumoniae infections. The proteins may also be used in the detection of
CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC DNA probe assay or blotting techniques for determining Chlamydia
CC pneumoniae gene expression. The present sequence represents a
CC specifically claimed Chlamydia pneumoniae protein of the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 928 AA;

Query Match 42.9%; Score 2048; DB 5; Length 928;
Best Local Similarity 46.5%; Pred. No. 1.4e-126;
Matches 442; Conservative 144; Mismatches 320; Indels 44; Gaps 20;
QY 1 MKSSPPKVPF-STFALF---PLSMIAETVVLSSASFGDNKN-GNFSVRESQEDAGTYYL 55
DB 1 MKSQSWLVSSTLACFTSCSTVFAATAENIGPSDSFDGNTGTYTPKNT--TTGIDYT 58
QY 56 FKGNVLENIPGTGTAITKSCFNNTKGLDFTGNGNSLLFQTVDACTVAGAAVNSVVDK 115
DB 59 LTGDITLQNL-GDSAALTGCFSDTTESLSFAGKGYSLFNLKIS-SAEGAAL-SVTTOK 115
QY 116 STTFGFSLSPTASPGSITT--GKGVSCSTGSLSTKYNSLLSKNFSTNGGAI 173
DB 116 NLSLTGFSLLTFLAAPSIVITTPSGKGVKCG--GLTDFDNNGTILPKQDYCEENGGAIST 174
QY 174 KTLSTLGTMTSALFSENTS---KKGAIQTSDALITIGNQGEVSFSDNTSSDGAIIFT 230
DB 175 KNLKNSKTSISFEGNKSSATCKGKAICATGTVITNTAPTLSNNIAEAGGAINS 234
QY 231 EASVTISNNAKVSFIDNKVTGASSSTGDMGSAICAYKTSSTDKVTLCGNOMLLFSNNT 290
DB 235 TGNCTITGNTSLVSENSVT---ATAG--NGGAL-----SGDADVTISGNSQVTFSGNQ 283
QY 291 SITTAGGAIYVKLELAS--GGLTFSRNSVNGCTAPKGAIAIEDSGELSLSDSGDIVF 348
DB 284 AVANGGAIYAKKUTLASGGGVSPFIIIVQGTAGNGGAISILAEGLSLSAEGDITF 343
QY 349 LGNTVTSSTP--GTVNRSSIDLTGSAKTAFLSAAGRAIFYDPTTGSSTTTVDLVKNET 407
DB 344 NGNAIVATTPQTTKNSIDIGSTAKITNLRAISGHSIFFYDPTTANTAADSTDTLNLKA 403
QY 408 PADSALQYTGNIITFTGKLESEADSKNLTSKLLQPVTLSSGGLTSLKHGVTLTQTQFTQ 467

DB 404 DAGNSTDYSGIVFSGEKLSDEAKVADNLSTLKPVTLLTAGNLVLKRGVTLDTKGFTQ 463
QY 468 QADGRLEMDVCTILEPA-DTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGFTILLD 526
DB 464 TAGSSVINDAGTTLKASTEVEVTLGLSPVDSLGEKKVIAAASAASXNVALSGPILLD 523
QY 527 PTGTFYENHSLRNPSQSYDILELKASGVTVSTAVTPDPIMGKFKHYGYGTWGPVW---- 582
DB 524 NQGNAYENHDLGKTQDFSFVQLSALGTATTTDPAVPTVATPTHYGYGTWGTW-MTWVDDT 582
QY 583 -GTGASTTATFNTKTGYIPNPERIGSLVPSNLSNAPRIDISSLHYLMETANEGLQGDRAF 641
DB 583 ASTPKTKTATLAWTNTGYLPNPEROGPLVPNSLMGSGFSDIQAIQGVIERSAITLCSDRGF 642
QY 642 WCAGLSNFFHKDSTKTRRGFRHLSSGYYVIGNLAHTCSDKILSAAPCQLFGRDRDYFAKN 701
DB 643 WAAGVANFLDKDKEKRYRKHSGYGAIGAAQTCSENLSISFAFCQLFGSKDFLVAKN 702
QY 702 QGTVVGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDNDLTKY 758
DB 703 HTDTYAGAFYIQH---ITECSGFTGCCLLDKLPGSWSHKPLVLEGLQLAYSHVSNLTKY 758
QY 759 TTYPTVKSGWNSDFALEFGGRAPICLDBESALFEOYMPMKLQFVVAHQEGFEQTEAR 818
DB 759 TAYPEVKGSGWNAFNMMLGASSHSYPEYLHCFDTYAPYIKLNTLYIRQDSFSEKTEGR 818
QY 819 EFGSRLVNLALPIGIRFEDKESDCQDATYNLTGYTVDLVRSPDCTTTTLRISGDSWKTF 878
DB 819 SFDDSNLNLNLSLPIGVKFEKESDCNDFSYDLTSLVVPDLIRNDPKCTTALVISGASWET 878
QY 879 GYNLAROALVLRAGNHCFNSNFEAFSPQSFELGRSSRNYYNVDLGAQYOF 928
DB 879 ANNLAQALQVRAGSHYAFSPMFVLQGFVFEVRGSSRIYNYVDLGGKFOF 928
RESULT 7
AA90237
ID AAY90237 standard; protein; 928 AA.
XX AC AAY90237;
XX DT 12-SEP-2003 (revised)
XX DT 29-AUG-2000 (first entry)
XX Chlamydia antigen CPN100635.
XX Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
XX therapy; upper respiratory tract disease; bronchitis; sinusitis;
XX asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.
XX Chlamydia pneumoniae.
XX Key Location/Qualifiers
XX Peptide 1..43 "signal peptide"
XX Protein 44..928
XX /note="mature CPN100635"
XX WO200032794-A2.
XX 08-JUN-2000.
XX 01-DEC-1999; 99WO-CA001147.
XX 01-DEC-1998; 98US-0110339P.
XX 01-DEC-1998; 98US-0110340P.
XX 01-DEC-1998; 98US-0110427P.
XX 01-DEC-1998; 98US-0110428P.
XX 01-DEC-1998; 98US-0110438P.
XX (CONN-) CONNAUGHT LAB LTD.
XX

PI Murdin AD, Oomen RP, Wang J;
 XX WPI; 2000-412339/35.
 DR N-PSDB; AAA30849, AAA30850.
 XX
 PT Nucleic acids encoding polypeptide antigens from Chlamydia useful for
 PT preventing, diagnosing and treating diseases such as community acquired
 PT pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
 PT asthma.
 XX
 PS Claim 16; Fig 3; 174pp; English.
 XX
 CC This sequence is a Chlamydia antigen of the invention, designated
 CC CPN100635. The nucleic acids (and their complementary sequences) may be
 CC used as diagnostic agents for detecting the presence of nucleic acids
 CC encoding Chlamydia antigens in samples according to standard methods, and
 CC therefore, for diagnosing Chlamydia infections. For example, they may be
 CC used as primers and probes for diagnostic polymerase chain reaction (PCR)
 CC assays. Antisense sequences may be used to down regulate expression of
 CC the proteins and may be used to treat infections. The nucleic acids may
 CC also be used to produce the protein antigens they encode according to
 CC standard recombinant DNA methodologies. The proteins may then be used as
 CC antigens for the production of antibodies (i.e. as vaccines) for
 CC preventing infection by Chlamydia. The antibodies may also be used as
 CC diagnostic reagents for detecting infections. Chlamydia is a pathogen
 CC implicated in the development of (for example) community acquired
 CC pneumonia, upper respiratory tract disease (especially bronchitis and
 CC sinusitis, asthmatic bronchitis, adult-onset asthma and acute
 CC exacerbations of asthma in adults. (Updated on 12-SEP-2003 to standardise
 CC OS field)
 XX
 XX Sequence 928 AA;

Query Match 42.3%; Score 2021; DB 3; Length 928;
 Best Local Similarity 46.1%; Pred. No. 8.5e-125;
 Matches 438; Conservative 142; Mismatches 326; Indels 44; Gaps 20;

QY 1 MKSSFFKFPV-STFAIF---PLSMIATETVLDSASPDGKKN-GNFSVRESQEDAGTTL 55
 DB 1 MKSQFWLVLSTLACFTSCSTVFATAENIGSDSFDGSTNGTYTPKNT--TTGIDYT 58
 QY 56 FKNVILENIPGTGTAITKSCFNNTKGLFTTNGNSLLFQTVDAAGVAGAAVNSSVVDK 115
 DB 59 LTGDTLQNL-GDAAATKGFCDTTESLSFAGKGYSLPLNKS-SAEGAAL-SVTTDK 115
 QY 116 STTFIGFSSLPSTASPGSSFTT--GKGAUSCTGSLSLTKVNSLLRSKNPSTNGAITA 173
 DB 116 NLSLTGFSLLFLAAPS SVITPSPGKGVKCG-GDITFDNNNGTILPKQDYCEENGGAIST 174
 QY 174 KTLSLGTGTTMSALFSENTSS--KKGGAIGTSDALITITGNGEVSPSDNTSSDGGAAIFT 230
 DB 175 KNLSLKNSTGISFEGNKSSATKKGGAICATGTVDTTNTATPLFSNNIAEAGGAINS 234
 QY 231 EASVTISNNAKVSFINKVTGASSSTGDMGGAI CAYKTSTDTKVTLTGQNQLMFLSNNT 290
 DB 235 TGNCITITGNTSLVFSNSVT---ATAG--NGGAL-----SGDADVTISGNQSVTFSGNQ 283
 QY 291 STTAGCAIYVKKLELAS--GGLTLFRNSVNGCTAPKGAIAIEDSGELSLSDSGDIYF 348
 DB 284 AVANGAIIYAKKLTLASGGGGNPNNNIVQGTAGNGGAISILAAGECSLFSAGDHYL 343
 QY 349 LGNTVISTTP-GTNRSSIDLGTSAKMTALRSAGRAIYFVDPITTGSSVTVDVLKNET 407
 DB 344 NGNAIVATTPTQTKRNSIDIGSTGKDHLELRASGHSIFPFDPTANTADSTDTLNKA 403
 QY 408 PADSALOYTGNIIPTGEKLSSEEAADSKNLTSLKLPVTLSGTSLKHGVTILQTAFTQ 467
 DB 404 DAGNSTDYSIGSVFSGEKLSEDEAKVADNLTSLKQPVTLTAGNLVLRGVTILDTKGFTQ 463
 QY 468 QADSRLMDVGTTLLEPA-DTSINNLVINISSIDGAKKAKIETKATSKNLTLSGTTLLD 526
 DB 464 TAGSSVIMDAGTTLKASTBEVTLTGLSIPVDSLGECKGVVIAASAASKNVALSGPILLD 523

QY 527 PTGTFYENHSLRNPSQSYDILELKASCTVTSTAVTDPDPMGEKPHYGYGTWGPVW---- 582
 DB 524 NQGNAYENHDLGKTQDFSFQLSALGTATTTDPAVPTVATPTHYGYGTWGTW-MTWVDDT 582
 QY 583 -GTGASTATTAFTNWTKTGYIPNPERIGSLVPSNLWNAFIDISSLHVLMTANEGLOGDEAF 641
 DB 583 ASPTKTTATLAWNTGYLPNPERQGPLVPSNLWGSFSDQAIQGVIERSAITLCSDRGF 642
 QY 642 WCAGLSNFFHKOSTKTRGRFRLHSGGVIYGNLHCTSDKILSAAFCQLFGRDRDYFVAKN 701
 DB 643 WAAGVANFLDKDKKGEKKYRHKSGGYAIGGAACTCSENLSFAFCQLFGSDKDFLAKN 702
 QY 702 QGTVYGCTLYXONNETYISLPCKLRPCSLSVVP---TEIPVLFSGNLSYHTDNDLTKTY 758
 DB 703 HTDTYAGAFYIQH----ITCSEFGICLLDKLPQSWSHKPLVLEGOLAYSHSVNDLTKTY 758
 QY 759 TTYPTVKGSGNDNSFALEFGGRAPICLDESALPQYMPFMKIQFYVAHOEGFEQGTTEAR 818
 DB 759 TAYFEVKGSGNNAFNMMGLGASSHSYPEYLHCFTYAPYIKLNTYIRQDSFSKGTGTR 818
 QY 819 EFGSSRLVNLALPIGIRFDKESQCDATYNTLTGYTVDLVRSNPDCTTTLRISGDSWKT 878
 DB 819 SFDDSNLFNLSPITGVKFEKFCNDPFSYDLTILSYVPDLIRNDPKCTTALVISGASW 878
 QY 879 GTNLARQALVLRAGNHCFNSNFEAFSQPSFELRGSSRNYNVDLGAKYQF 928
 DB 879 ANNLAQALQVRAGSHYAFSPMEFVLGQFVFEVRGSSRIYNVDLGGKQF 928

RESULT 8
 AAY69369
 ID AAY69369 standard; protein; 918 AA.
 XX
 AC AAY69369;
 XX
 DT 12-SEP-2003 (revised)
 DT 19-JUN-2000 (first entry)
 XX
 DE Amino acid sequence of the CPN100395 polypeptide.
 XX
 KW CPN100395; Chlamydia infection; immune response; vaccine.
 XX
 OS Chlamydia pneumoniae.
 XX
 PN W020001183-A2.
 XX
 PD 02-MAR-2000.
 XX
 PF 18-AUG-1999; 99WO-IB001449.
 XX
 PR 20-AUG-1998; 98US-0097187P.
 PR 20-AUG-1998; 98US-0097188P.
 PR 20-AUG-1998; 98US-0097189P.
 PR 20-AUG-1998; 98US-0097190P.
 PR 20-AUG-1998; 98US-0097195P.
 PR 20-AUG-1998; 98US-0097196P.
 PR 20-AUG-1998; 98US-0097197P.
 PR 27-AUG-1998; 98US-0097191P.
 PR 17-AUG-1999; 99US-00376770.
 XX
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 PI Murdin AD, Oomen RP;
 XX
 DR WPI; 2000-224703/19.
 DR N-PSDB; AA261509.
 XX
 PT Novel antigens and corresponding DNA molecules that can be used to
 PT prevent, treat and diagnose disease caused by Chlamydia infection in
 PT mammals, especially humans.
 XX
 PS Claim 19; Fig 15-E; 201pp; English.

PI Murdin AD, Oomen RP, Wang J;
XX WPI; 2000-412339/35.
DR N-PSDB; AAA30849, AAA30850.
DR
XX Nucleic acids encoding polypeptide antigens from Chlamydia useful for
PT preventing, diagnosing and treating diseases such as community acquired
PT pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
PT asthma.
XX
PS Claim 16; Fig 3; 17app; English.
XX
XX This sequence is a Chlamydia antigen of the invention, designated
CC CPN100635. The nucleic acids (and their complementary sequences) may be
CC used as diagnostic agents for detecting the presence of nucleic acids
CC encoding Chlamydia antigens in samples according to standard methods, and
CC therefore, for diagnosing Chlamydia infections. For example, they may be
CC used as primers and probes for diagnostic polymerase chain reaction (PCR)
CC assays. Antisense sequences may be used to down regulate expression of
CC the proteins and may be used to treat infections. The nucleic acids may
CC also be used to produce the protein antigens they encode according to
CC standard recombinant DNA methodologies. The proteins may then be used as
CC antigens for the production of antibodies (i.e. as vaccines) for
CC preventing infection by Chlamydia. The antibodies may also be used as
CC diagnostic reagents for detecting infections. Chlamydia is a pathogen
CC implicated in the development of (for example) community acquired
CC pneumonia, upper respiratory tract disease (especially bronchitis and
CC sinusitis, asthmatic bronchitis, adult-onset asthma and acute
CC exacerbations of asthma in adults. (Updated on 12-SEP-2003 to standardise
CC OS field)
XX
SQ Sequence 885 AA;
Query Match 41.6%; Score 1987.5; DB 3; Length 885;
Best Local Similarity 46.9%; Pred. No. 1.3e-122;
Matches 420; Conservative 136; Mismatches 302; Indels 37; Gaps 16;
QY 51 GTTYLFGKGVNLENTPGTGTATKSCFNNTKGDLPFTGNGSLLFQTVDAAGTVAGAAVNS 110
DB 11 GIDYTLTGDTLQNL-GDSAAITKGCFTDTSLSFAGKGYSLSFNINIKS-SAEAGAL-S 67
QY 111 SVVDKSTTFIFGFSLSFIASPGSSIT--GKGAIVCSCTGSLSLTKNLSLLFKNFSTDNG 168
DB 68 VTTDKNLSLTGFSSTLFLAAPSIVITPSGKAVKCG-GDLTFDNNGTILFKQDYCEENG 126
QY 169 GAITAKTSLTGTMTSALESENTSS---KKGAIQTSALTITGNGGVSFSDNTSSDSG 225
DB 127 GAISTKNLSLKNSTGSGISFEGNKSSATGKGAICATGTVDTITNTAPTILFSNNIAEAG 186
QY 226 AAIPTASVTISNNKAVFIDNKVTCASSSTTGDMSGGAIKAVKTSKTDKVTILTGQMLL 285
DB 187 GAINSTGNCITITGNTSLVFSNSVT---ATAG--NGGAL-----SGDADVTISGNSQSVT 235
QY 286 FSNNTSTTAGGAIYVKKLELAS--GGITLFSRNSVNGTAPKGAJAIEDSGELSLSADS 343
DB 236 FSGNQAVANGGAIYAKKILASGGGNGFPNNIVQGTAGNGGALSILAAEGCSLPSEA 295
QY 344 GDIVFLGNTVTSTTP-GTNRSSIDLTSKAMTALRSAGRAIYFYDPIITGSSSTVTDVL 402
DB 296 GDHYLNGNAIVATTPQTTKNSIDIGSTGKDHLEIRAISSHSIFFYDDPITANTADSDTTL 355
QY 403 KVNETHPADSALQVTGNIITFGEKLSSETAADSNNLSKLLQPVTLTSGTTLSLKHGVTLOT 462
DB 356 NLNKADAGNSTDYSGSIVFSGEKLSEDEAKVADNLNLSLTQPVTLTLAGNLVLRGVTLD 415
QY 463 QAPTQQADSRLEMDVGTTLLEPA-DTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGT 521
DB 416 KGTQTAGSVIMDAGTTLKASTEEVTLTGLSPVDSLGEKGVVIAAASAKNVALSGP 475
QY 522 ITLLDPTGTFTYENHSLRNPOSYDILELKASGTVTSTATPDPIMGEKPHYGQGTWGPV 581
DB 476 ILLLDNQNAYENHDLGKTQDFSFVQLSALGTATTTDVPVATPTVATPHYGQGTWGT-MT 534

QY 349 LGNTVTSTTP-GTVRRSSIDIGTSKMTALRSAGRAIYFYDPIITGSSSTVTDVLKVNET 407
DB 344 NGAIVATTPQTTKRNISIDIGSTAKITNLRAISGHSIFFYDPIITANTAAADSTDLNKA 403
QY 408 PADSALOYTGNIIFTGEKLSSTEADSKNLSKLLQPVTLTSGGTLKSHGVTLOTAFTQ 467
DB 404 DAGNSTDYSGSIVFSGEKLSEDEAKVADNLNLSLTQPVTLTLAGNLVLRGVTLOTGPTQ 463
QY 468 QADSRLEMDVGTTLLEPA-DTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLD 526
DB 464 TAGSVIMDAGTTLKASTEEVTLTGLSPVDSLGEKGVVIAAASAKNVALSGPILLD 523
QY 527 PTGTFYENHSLRNPOSYDILELKASGTVTSTATPDPIMGEKPHYGQGTWGPVW---- 582
DB 524 NQGNAYENHDLGKTQDFSFVQLSALGTATTTDVPVATPTVATPHYGQGTWGTWVVD 582
QY 583 -GTGASTTATFNWTKTIGYIPNPERIGSLVPSNLMNAFIDISLHYLMETANEGLQDRAP 641
DB 583 ASTPKTKATLANWTGVLNPNRGQPLVPSNLMGFSFDIQAIOGVRSALTLCSDRGF 642
QY 642 WCAGLSNFHKDSTKTRGFRHLSCGYVIGMHLTCSKILSAARCOLFGRDRDYFVAKN 701
DB 643 WAAGVANFLDKDKGKRYKHSKGYAIGGAAQTCSENLTSPAFCOLFGSKDFLVAKN 702
QY 702 QGTVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDNDLTKY 758
DB 703 HTDTYAGAFYIQH----ITECSGFTGLCDKLPLGWSHKPLVLEQLAYSHVSNLTKY 758
QY 759 TTYPTVKGSGWNSDALEFGGRAPICLDESALFEQYMPFMKLFQVYAHQEGFKEQTEAR 818
DB 759 TAYPEVKSNGWNAFNMMLGASHSYPEYLHCFDIYAPYIKLNTLYIRQDSFSEKTEGR 818
QY 819 EFGSRLVNLALPIGRFDKESCDQATNLTLYGTVDLVRNPDCTTILRISGDSWTF 878
DB 819 SFDDSNLFLSLPIGVKFEKFSKDNDFSYDLTSLYVPDLIRNDPKCTTALVISGASWET 878
QY 879 GTNLARQALVLRAGNHCFNSNFEAPSFPSFELRGS 914
DB 879 ANNARQALQVRAGSHYAFSPMEVLGQFVFEVRGS 914
RESULT 11
AA190238
ID AAY90238 standard; protein; 885 AA.
AC
XX
XX AAY90238;
DT 12-SEP-2003 (revised)
DT 29-AUG-2000 (first entry)
DE
XX Mature Chlamydia antigen CPN100635.
XX Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
XX therapy; upper respiratory tract disease; bronchitis; sinusitis;
KW asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.
XX
OS Chlamydomphila pneumoniae.
XX
XX WO200032794-A2.
XX
XX 08-JUN-2000.
XX
XX 01-DEC-1999; 99WO-CA001147.
XX
XX 01-DEC-1998; 98US-0110339P.
XX 01-DEC-1998; 98US-0110340P.
XX 01-DEC-1998; 98US-0110427P.
XX 01-DEC-1998; 98US-0110428P.
XX 01-DEC-1998; 98US-0110438P.
XX
XX (CONN-) CONNAUGHT LAB LTD.

582 W-----GTGASTTATFNWTKTYIPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLO 636
 535 WVDSTASTPKTKATLATWNTGYLPNPERQGPLVPSNLWGSFSDIQAIGVIERSAULTIC 594
 637 GDRAFWCAGLSNFHDKSTKRRFRHLISGGYVIGGNLHTCSDKILSAAPQLFRDRDY 696
 595 SDRGFWAAGVANFLDKDKGKRYRKSGGYAIAGAAQTCSENLIISFAFCQLFGSKDF 654
 697 FVAKNOCTVYGGTLYYQHNETYIISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDND 753
 655 LVAKNHTDTVAGAFYIOH----ITECGFTICLLDKLPGWSHKLPLVLEGQLAYSHVSDND 710
 754 LKTKYTYPTVKGSGWNSDFALEFGGRAPICLDESALFEQYMPFMKLQFYVAHQEGFKEQ 813
 711 LKTKYTAYPEVKGSGWNAFMNLGASSHSYPEYLHCFDTPYVYIKLNLYIRODSFSEK 770
 814 GTEAREFGSSRLVNLALPIGIRPEKESDCQDATYNLILGYTVDLVRNPDCTTTLRISGD 873
 771 GTEGRSDDSNLFLNLSUPIGVKFEKESDCNDSDYDLTSLYVPDLIRNDPKCTTALVISGA 830
 874 SWKTFGNLARQALVLRAGNHFCFNSNFEAFQSFELRGSSRNYYNVDLGAKYOF 928
 831 SWETYANNLARQALQVPRAGSHYAFSPMFEVLQGFVEVRGSSRIYVNDLGKPOF 885

RESULT 12

AAW88423
 ID AAW88423 standard; protein; 928 AA.

AC AAW88423;
 XX
 DT 17-OCT-2003 (revised)
 DT 26-APR-1999 (first entry)

XX Chlamydia pneumoniae surface exposed protein Omp10.

XX Omp10; outer membrane protein 10; surface exposed protein; antigen;
 KW infection; diagnosis; vaccine; atherosclerosis; asthma.

XX Chlamydia pneumoniae.

XX WO9858953-A2.

XX 30-DEC-1998.

XX 19-JUN-1998; 98WO-DK000266.

XX 23-JUN-1997; 97DK-00000744.

XX (BIRK/) BIRKELUND S.

PA (CHRI/) CHRISTIANSEN G.

XX Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;

XX WPI; 1999-105610/09.

DR N-PSDB; AAX06822.

XX Species-specific test for identifying mammals infected with Chlamydia
 PT pneumoniae - comprises detecting antibodies specific for outer membrane
 PT proteins of C. pneumoniae or nucleic acids encoding these proteins.

XX Claim 7; Page 60-62; 115pp; English.

XX This polypeptide comprises the novel 98.4 kDa surface exposed protein
 CC Omp10 of the human respiratory pathogen Chlamydia pneumoniae. Its amino
 CC acid sequence was deduced from DNA (see AAX06822) isolated from a C.
 CC pneumoniae expression library. The invention provides 12 novel surface
 CC exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid
 CC sequences encoding them (see AAX06816-27). A new species specific test is
 CC claimed that is used to identify mammals (including humans) infected with
 CC Chlamydia pneumoniae. The test comprises detecting antibodies specific
 CC for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
 CC membrane proteins, especially by PCR. The proteins are also used in the

CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids and
 CC proteins can also be used in the immunization of mammals, the nucleic
 CC acids being particularly useful as DNA vaccines for affecting in vivo
 CC expression of antigens. The vaccines may also prevent atherosclerosis and
 CC bronchial asthma, which are possibly associated with C. pneumoniae.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 928 AA;

Query Match 41.6%; Score 1986; DB 2; Length 928;
 Best Local Similarity 45.3%; Pred. No. 1.8e-122;
 Matches 430; Conservative 149; Mismatches 327; Indels 44; Gaps 19;

QY 1 MKSFPKPFVSTFAIFPLSM-----IATETVLDSSASFQNGKNGFSVRESQEDA-GTT 53

Db 1 MKSLHWFVSSSLALPLSLNFSAFAVVEINLGPNTNSFSG--PGTYTPPAQTINADGTI 58

QY 54 YLFKGNVTLENIPTGTAITKSCFNNTKGDLTFTGNGNSLLFOTVDAGTVAGAAVNSVV 113

Db 59 YNLTDGVSITN-AGSPALTATSCFETTGNSLFGHGYQFLLQNLIDAG--ANCTFTNTAA 115

QY 114 DKSTTFGFSLSFIASPGSSITTKGAVSCSTGSLTKNLSLLFSKNFSTONGGAITA 173

Db 116 NKLLSFGSGLSLIQT--TNATTGTGAIK-STGACSIQSNYSYCFQNFNDNGALQ 172

QY 174 KTLSLTCTMSALFSENTSSKKGAIQTSDALITIGNQGEVSFSDNTSSSGAAIFTEAS 233

Db 173 SSISLS-LNPNLTFAKNKATQKGALYSTGGITINNTLSASFSENTPAANGGAIYTEAS 231

QY 234 VTISNNAKVSFIDNKVTGASSSTTGMDSGCAICAYKTSTDTKV-TLTGNQMLFSNNTST 292

Db 232 SFISSNKATSFINNVTATSA-----TGGAIVCSSTSPKPVLTLLSDNGELNFIQNTAI 285

QY 293 TAGGAIYVKKLELASGCLTLFSRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNT 352

Db 286 TSGGAIYTDNLVLSGGPTLFKNNSALDTPALGGAIADSGSLSLALGGITFEGNT 345

QY 353 V---TSTTGTNRSSIDLG-TSAKMTALRSAAGRAIYFYDPIITGSGSTTVTDVLKNETP 408

Db 346 VVKGASSQTTTNRNSINIGNTNAKIVQLRASQNTIIFYDPIITTNHTAALSDALNLGPD 405

QY 409 ADSALQYTGNIIFTGEKLSATEAADSCKNLTSKLLQPVTLSSGGLSLKHGVTLOQTQFTQ 468

Db 406 LAGNPAYQGTIVPSGEKLSAEAEADNLKSTIQQLTLTAGGQLSKSGVTLLVAKSFSQS 465

QY 469 ADSRLEMDVGTLEPADTSTINNLVINISSIDGAKKAKIETKATSKNLISGTTILLDPT 528

Db 466 PGSTLLMDAGTTLETADGITINNLVNLVDSLKTKKATLKATQASQTVTLSSGLSLVDPS 525

QY 529 GTFYENHSLRNPSQSYDILELKAS--GTVTSTAVTPDPIMGEKPHYGYQGTWGVVWGTA 586

Db 526 GNVYEDVSWNNPQVFSCLTLTADDPANIHITLADADPLEKPIHWGYQGNWA-LSWQEDT 584

QY 587 ST---TATFNWTKTYIPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGQDRAFWC 643

Db 585 ATKSKAATLTWTKGYNPNPERRGTLVANTLWGSFVDVRSIQQLVAIKVRSQSETGIWC 644

QY 644 AGLSNPFHKDSTKTRRGFRHLISGGYVIGGNLHTCSDKILSAAPQLFRDRDYFVAKNOG 703

Db 645 EGISNPFHKDSTKINKGPRHISAGYVVGATTTLASDNLITAAFCQLFGKDRDHFINKRA 704

QY 704 TVYGGTLYYQHNETYIISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDNDLTKYTT 760

Db 705 SAYAAHLHLOHLATLSS-----PSLLRYLPQSESEQPVLFDAQISYIYKNTMTKTYTQ 758

QY 761 YPTVAGSGWNSDFALEFGGRAP-ICLDESALFEQYMPFMKLQFYVAHQEGFKEQTE-AR 818

Db 759 APKGSWYNDQCALELASSLPHTLSHGLEPHATFPPIKVEASTIHQDSFPERNTLVR 818

QY 819 EFGSRLVNLALPIGIRPEKESDCQDATYNLILGYTVDLVRNPDCTTTLRISGDSWKT 878

Db 819 SFDSDGLINVSPIGTFIFERFSRNERASYEATVIYVADYRKNPDPCTTALLINNTSWKIT 878

Qy	879	GTNLARQALVLRAGNHFCFNSNFEAFSOFSEFLRGSSRNNYVDLGAKYQF	928
		: : : : : : :	
Db	879	GTNLSRQAGICRAGIFYAFSPNLEVTSNLSWEIRGSSRSRYNADLGGKFFQ	928

RESULT 13
ABB90542
ID ABB90542 standard; protein: 928 AA.

AC ABB90542;

29-AUG-2003 (revised)

DI 2002-2003 (1155 CIRC),
XX

DE CHLAMYDIA PNEUMONIAE CP0/31 protein, SEQ ID NO:33
yy

Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW
human respiratory disease; cardiovascular disease; atherosclerosis;
KW
coronary artery disease; carotid artery stenosis; myocardial infarction;
KW
cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW
strain CWM029.

OS Chlamydophila pneumoniae.

XX	Key	Location/Qualifiers
FH		

FT	Peptide	1.	.26

FT	/label= Signal_peptide
05	000
06	000
07	000
08	000
09	000
10	000
11	000
12	000
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99	000
100	000

PT	Protein	27. .928	/note= "Mature protein"
PM			

XX
FI 1000- / Machine Problem

PN WO200202606-A2.

10-JAN-2002.

03-JUL-2001: 2001WO-IB001445.

03-JUL-2000: 2000GB-00016363.

PR 11-JUL-2000; 2000GB-00017047.

PR 21-JUL-2000; 2000GB-00017983.

PR 07-AUG-2000; 2000GB-00019368.

PR 18-AUG-2000; 2000GB-00020440
PR 14-SEP-2000; 2000GB-00022583

PR 10-NOV-2000; 2000GB-00027549.

PR 22-DEC-2000; 2000GB-00031706.

	6	XX
	7	XX

PA (CHIR-) CHIRON SPA.
 VV

Ratti G, Grandi G;

XX

DR WPI; 2002-154726/20

DR N-PSDB; ABL91200.
vv

Novel *Chlamydia pneumoniae* protein useful in the manufacture of a medicament for treatment or prevention of infection due to *Chlamydia*, preferably *Chlamydia pneumoniae*, and for diagnostic purposes.

XX
pg
claim 1: Page 57: 364nn: English:

Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWI029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carotid artery stenosis, myocardial infarction, cerebrovascular disease, aortic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched DNA probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a

U U

CC	specifically claimed Chlamydia pneumoniae protein of the invention.
CC	(Updated on 29-AUG-2003 to standardise OS field)
XX	
QQ	Sequence 928 AA;
	Query Match 41.5%; Score 1982; DB 5; Length 928;
	Best Local Similarity 45.28; Pred. No. 3.3e-122;
	Matches 429; Conservative 150; Mismatches 327; Indels 44; Gaps 19;
QY	1 MKSFPKFFVFSTFAIFPLSM-----IATETVLDSSASFDGNKNGNPSFVRESQEDA-GTT 53
DB	1 MKSLHWFLISSSLALPLSLNFSFAFAVVEINLGPNTSPFSG--PGTTPPAQTINADGTI 58
QY	54 YLFKGNVTLENIPTGTATITKSPNNNTKGDITFTGNGNSILLPQTVDAGTVAGAAVNSVV 113
DB	59 YNLTDGVSITN-AGSPALTATSCFKETITGLNLSFGHGQYQLLOWIDAG--ANCTFTNTAA 115
QY	114 DKSTTFEGFSSLPFASPGSITTKGAVSCSTGSLSLTKNVSLFKNFSTDMNGAITA 173
DB	116 NKLUSFGFSLSLIQT--NATITGTGAIK-STGACSIQSNYSYCFQGNFNDNGGALQG 172
QY	174 KTLISLTGTTMSALPESNTSSKKGAIQTSDALTTITNGQEVSPSDNTSSDSGAAIPTFAS 233
DB	173 SSISLS-LNPNLTAKNKATQKGALYSTGGITINNTLNGASFSEFNTAANGGAIYTEAS 231
QY	234 VTISNNAKVSPIDNKVTGASSITTCGDMSGGAI CAYKTTSTDKV--TLTGNQMLFESNNTST 292
DB	232 SFISNNKAISFINNSVTATSA-----TGGAIYCSSTAPKPVLTLSNGELNFINGTAI 285
QY	293 TAGGAIYVKKLELASGGTLTFSRNSVNGTAPKGAIAIEDSGBELSLASDSGDIVFLGNT 352
DB	286 TSGGAIYTDNLVLSSGGPTLPFNNSAIDTAAPLGAIALADSGSLSALSGDITFEENT 345
QY	353 V---TSTPTGPNRRSIDLG-TSAKMTALRSAGRAIYFYPDITGSSSTVTVDVLKVNTP 408
DB	346 VVKGASSQTTRNSINIGNTNAKIVQLRASQGNITFYDPTTITSITAAALSDALNNGPD 405
QY	409 ADSALQYTCNLIIFTEKELSETEADSKNLTSKLLQPVTLTSGTISLKHGVTLOTQAFTQQ 468
DB	406 LAGNPAYQGTIVFGEKLESEAAEADNLKSTIQOPLTAGGQJLSKSGVTILVAKSFQS 465
QY	469 ADSRLEMDVGTLEPADTSTNNLVINISIDGAKAKIETKATSKNLTLSGTITLLDPT 528
DB	466 PGSTLLMDAGTLETADGITINNLVNLVNDLSLKETKKATLKATQASQVTLTSGSLSDVPS 525
QY	529 GTFYENHSLRNPQSYDILLELKAS--GTVSTAVTPDDPMGKEFHYGYQGTGPIVWGTCGA 586
DB	526 GNVYEDVSWNNPQVFSCLTLTADDPANHIITDLAADPLEKNP IHWGYQGNWA-LSWQBDT 584
QY	587 ST---TATFNWTKTYINPERIGSLVPSNLWNAFIDISLHYLMETANEGLQGDRAFWC 643
DB	585 ATKSKAATLTWTKGYNPNPERRGFLVANTLMGSLFVDRSIOQLVATKVRQSQETRGWIC 644
QY	644 AGLSNFFHKDSTKTRRGFRHLSGGYVIGNLHTCSDKILSAAFCOLPGRDRDYFVAKNQG 703
DB	645 EGLSNFFHKDSTKINKGFRPHISAGYVVGATTTLASDNLITAAFCOLFGKDRDHFINKNRA 704
QY	704 TVYGTGLTYQHNETHYISPCUKLRPCSLSVTP---TEIPVLPSGNLSYTHTDNDLTKYTT 760
DB	705 SAYAASLHLQLATLSS-----PSILRLYLPQSESEQPVLPDAQISYISKNTMKTYITQ 758
QY	761 YPTVKGWNGNDSFALFEGGRAP-ICLDESALPEQYMPFMKLOFVYAHQGFKEQGT-AR 818
DB	759 APKGSSWYNDGCAELASLSLPHALSHGLFHAFPPFIKVEASVYHQDSFERNTTLVR 818
QY	819 EFGSSRLVNLALPIGIRFDKESDCDQATYNLTGYTVDLIVRNSPDCITTLRLISGDSWKTF 878
DB	819 SPDSGDLINVSVPIGITTFERSRNERASYEATVIYVADYVRKNPDCITALLINNTSMKTT 878
QY	879 GTNLARQALVLRAHNHFCNFSNFEAFSQFSFELRGSSRNYYVDLGAKYQF 928
DB	879 GTNLSRQAGTGRAGIYFATSPNLEVTSNLSMEIRGSSRSINADLGKQFQF 928

KW vaccine; antibacterial; community acquired pneumonia; bronchitis;
KW sinusitis; acute respiratory disease; upper respiratory tract disease;
KW asthma; atherosclerosis.
XX Chlamydophila pneumoniae.
XX Key Location/Qualifiers
PH 1..11
FT Peptide /label= Signal_peptide
FT Protein 12..936
FT /label= 98_kDa_membrane_protein
XX WO200032784-A1.
XX
XX
XX PD 08-JUN-2000.
XX PF 01-DEC-1999; 99WO-CA001148.
XX PR 01-DEC-1998; 98US-0110439P.
XX PR 03-MAY-1999; 99US-0132272P.
XX
XX PA (CONN-) CONNAUGHT LAB LTD.
XX Murdin AD, Oomen RP, Wang J, Dunn P;
XX MPI; 2000-412330/35.
XX DR N-PSDB; AAA48838, AAA48839.
XX
XX New polynucleotide encoding the Chlamydia 98 kilodalton outer membrane
XX protein, useful for preventing or treating Chlamydia infection.
XX Claim 16; Fig 1; 98pp; English.
XX
XX The present sequence is CPN100640, the 98 kDa outer membrane protein from
XX Chlamydia pneumoniae. Chlamydia pneumoniae is a common cause of community
XX acquired pneumonia and upper respiratory tract symptoms and diseases,
XX including bronchitis and sinusitis. It also has an association with
XX atherosclerosis and asthma. The 98 kDa outer membrane protein is a C.
XX pneumoniae-specific antigen which can confer immune protection against
XX Chlamydia infection. The nucleotide sequence encoding the protein or the
XX protein itself may be administered as a vaccine to prevent or treat
XX infection and they may also be used to diagnose infection. The gene
XX encoding CPN100640 was amplified from Chlamydia pneumoniae genomic DNA by
XX PCR. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 936 AA;

Query Match 41.2%; Score 1965; DB 3; Length 936;
Best Local Similarity 43.4%; Pred. No. 4.4e-121;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;

QY 1 MKSSPFKVFSTPAIF-PLSMATEVTLDS-ASFDGKNGNFSVRESOE-DAGTTLFK 57
DB 1 MKSSVSWLFFSSIPFSSISVAARVTLDSNNNSYDGSNGTTFVSTTDAAGTYSLL 60

QY 58 GNVLTENIPGTGTAITKCFNNKGBLTFTGNGNSLLFOTVDAGTVAGAAVNSVVDKST 117
DB 61 SDVSFQAGALGIPLASGCFLEAGDLITFCQNHALKFAFINAGSAGTVASTAADKNL 120

QY 118 TFIGFSLSFIAPSGSSIT-TGKAVSCSTGSLTKQVSLFLPSKNPSTDNGAIAKTL 176
DB 121 LFNDFSLSLIISCPILLSPTGCALK-SVGNLSLTGNSQIIIFTONFSDNGGVINTKNF 179

QY 177 SLTGTMTSLFSENT--SSKKGAIQTSDALITGNGEVSFSDNTSSDSGAALFTEASV 234
DB 180 LLSGTSQFASFRNQAFPTGQGVVYATGTTITNSPGVFSQNLAKGGGALYSTDNC 239

QY 235 TISNAKVSFTDNKVTGASSSTTGDMSSGAICAYKSTDTKVTLTGNQMLLFSNNTSTA 294
DB 240 SITDNFQVIFDGNSAWEAQA-----QGAICCC-TTIDKVTLTGNKLSFTNNTALTY 292

QY 295 GGAIYVKKLEIASGGLTIFSRNSVNGGTAPK--GGAIAIEDSGELSLSDSGDIVFLGNT 352

Db 293 GGATSGLKVSISAGGPTLFSQN-ISGSAGOGGGGAINIASAGELALSATSGLDITFNNNQ 351
QY 353 VTSTTPGTNRSSIDLGTSAKMTALRSAGRAIYFYDPITTGSSSTVTDVLKVNTPPADSA 412
Db 352 VTNGSTST-RNAINI IDTAKVTSIRAAATGQSIYFVDPITNPGTAASTDTLNLADANSE 410
QY 413 LOYTGNIIFPGEKLSSETAADSKNLTSKLLOPVTLSGGTSLKHGVTLOTQAFQQAQDSR 472
Db 411 IEYGGAIVFSGEKLSPEKAIAANVTSTIROPVAVLRGDLVLRDGVTVTFKDLTQSPGSR 470
QY 473 LEMDVGTTLLEPADTS-TINNIVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTF 531
Db 471 ILMDGGTTLTSAKEANLSUNGLAVNLSSLDGTNKAAKTEAADKNLSLSTIALIDTEGSF 530
QY 532 YENHSLRNPOQSYDILEK---ASGTVTSTAVTPPIMGEKPHYGQGTWGIWGTGAST 588
Db 531 YENHLSKASTYPLLELTTAGANGTITLQALSTLTQEPETHYGYQGNW-QLSWANATSS 589
QY 589 -TATFNWTKGYIIPNPERIGSIVPNSLWNAIDIDISSLHYLMETANEGLQGDRAFWCAGLS 647
Db 590 KIGSINWTRTGYIPSPERKSNLPLNSLWGNFIDIRSINQLIETKSSGPPFERELWLSGIA 649
QY 648 NFEHKDSTKTRRGPRHLSGGYVIGGNLHTCSDKILSAAFCQLFGDRDRDYFVAKNQGTVYG 707
Db 650 NFFRDSNPTRHGPRHISGGYALGITATTPAEDQLTFAFCQLFARDRNHITGKNHGDYTG 709
QY 708 GTLYYQHNETYISLPCKL-----RPSLSVVPTEIPVLFSGNLSYTHTDNDLTKYTTY 761
Db 710 ASLYPHHTTEGLFDIANFLWKGKATRAPVWLSEISQIPLSFDAKFSYLTHTDNHMKYTYDN 769
QY 762 PTVKSGWNSDFALFEGGRAPICLDESALFEQYMPFMKLQFYVAHOEGFKEQGTAREFG 821
Db 770 STIKGSWRNDAPCADLGASLPFVTSVPVLLKEVEPFVKQYIYAHQQDFYERHAEGRAN 829
QY 822 SSRLVNLALPIGIRFDKSDCODATYNTLTGYTVDLVRSPDCTTTTLRISGDSWKTFTGN 881
Db 830 KSELINVELPIGVTERDSKSEKGYDITLWILDAYRNPCKQTSLIASDANMMAYGTN 889
QY 882 LARQALVLRAGNHCFNSNFEAFSFPSELGRSSRNYNVDLAKYQF 928
Db 890 LARQGSFVRAAHNFQVNPHEIFGQFAFEVRSRRNNTNLGSKFCF 936

Search completed: August 10, 2004, 13:12:55
Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:11:51 ; Search time 23 seconds
(without alignments)
2082.996 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSSFPRVFSTFAIFPLSM.....FELGSRNRYNVDLAKYQF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2802.5	58.7	597	4	US-09-198-452A-29
2	1940	40.6	930	4	US-09-198-452A-470
3	1917.5	40.2	927	4	US-09-198-452A-472
4	1856	38.9	949	4	US-09-198-452A-478
5	1572.5	32.9	643	4	US-09-198-452A-474
6	1417.5	29.7	922	4	US-09-198-452A-15
7	1377.5	28.9	973	4	US-09-430-723-2
8	1259	26.4	671	4	US-09-198-452A-468
9	1214	25.4	230	4	US-09-198-452A-30
10	1203.5	25.2	507	4	US-09-198-452A-32
11	1130	23.7	1132	4	US-09-198-452A-466
12	1128	23.6	1012	4	US-09-612-402B-2
13	1126.5	23.6	1006	4	US-09-556-877-190
14	1126.5	23.6	1006	4	US-09-620-412C-190
15	1126.5	23.6	1006	4	US-09-598-419-190
16	1124.5	23.6	982	4	US-09-556-877-176
17	1124.5	23.6	982	4	US-09-620-412C-176
18	1124.5	23.6	982	4	US-09-598-419-176
19	1117.5	23.4	984	4	US-09-612-402B-43
20	1110.5	23.3	1013	4	US-09-612-402B-15
21	1098.5	23.0	1013	4	US-09-612-402B-16
22	1015.5	21.3	450	4	US-09-612-402B-35
23	888	18.6	530	4	US-09-198-452A-482
24	865	18.1	880	4	US-09-556-877-175
25	865	18.1	880	4	US-09-620-412C-175
26	865	18.1	880	4	US-09-598-419-175
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28      856 17.9      866 4 US-09-620-412C-189      Sequence 189, App
29      856 17.9      866 4 US-09-598-419-189      Sequence 189, App
30      834.5 17.5      483 4 US-09-198-452A-27      Sequence 27, Appl
31      821 17.2      494 4 US-09-198-452A-33      Sequence 33, Appl
32      792 16.6      427 4 US-09-198-452A-31      Sequence 31, Appl
33      768 16.1      177 4 US-09-198-452A-28      Sequence 28, Appl
34      708 14.8      294 4 US-09-198-452A-469      Sequence 469, App
35      685.5 14.4      931 4 US-09-427-533B-2      Sequence 2, Appl
36      680.5 14.3      1617 4 US-09-198-452A-1035      Sequence 1035, App
37      667 14.0      1146 4 US-09-198-452A-580      Sequence 580, App
38      646 13.5      969 4 US-09-198-452A-501      Sequence 501, App
39      603.5 12.6      940 4 US-09-198-452A-500      Sequence 500, App
40      582 12.2      1530 4 US-09-556-877-178      Sequence 178, App
41      582 12.2      1530 4 US-09-620-412C-178      Sequence 178, App
42      582 12.2      1530 4 US-09-598-419-178      Sequence 178, App
43      559 11.7      1752 4 US-09-556-877-180      Sequence 180, App
44      559 11.7      1752 4 US-09-620-412C-180      Sequence 180, App
45      559 11.7      1752 4 US-09-598-419-180      Sequence 180, App

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ALIGNMENTS

RESULT 1
US-09-198-452A-29
; Sequence 29 Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:

; APPLICANT: Griflais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention of infection and treatment of infection

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 29

; LENGTH: 597

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-29

Query Match 58.7%; Score 2802.5; DB 4; Length 597;
Best Local Similarity 93.8%; Pred. No. 2.4e+204;
Matches 560; Conservative 5; Mismatches 21; Indels 11; Gaps 3;

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QY      149 LSLTKNVSLFKNFSTDNCGAIIAKTSLTGTMSALFSENTSSKKGAIQTSALTIT 208
Db      1 LEFDKNVSLFKNFSTDNCGAIIAKTSLTGTMSALFSENTSSKKGAIQTSALTIT 60

QY      209 GNGGEVSFSDNTSSDGAIIFTASVTISNNAKVSIIDNKVTGASSSTTGDMSGGAICAY 268
Db      61 GNGGEVSFSDNTSSDGAIIFTASVTISNNAKVSIIDNKVTGASSSTTGDMSGGAICAY 120

QY      269 KTSTDTKVTLTGNQMLFNSNTSTTAGGAIYKYLELASSGLTLFSRNVNGTAPKGA 328
Db      121 KTSTDTKVTLTGNQMLFNSNTSTTAGGAIYKYLELASSGLTLFSRNVNGTAPKGA 180

QY      329 IAIEDSGELSLSDSGDIVFLGNTVTSITPGNRSIDLTGSAKMTALRSAGRAIYFYD 388
Db      181 IAIEDSGELSLSDSGDIVFLGNTVTSITPGNRSIDLTGSAKMTALRSAGRAIYFYD 240

QY      389 PITGSSSTVTVLKVNETPADSALQYTGNIIFTGKLSSETAADSKNLTSKLLQPVTLIS 448
Db      241 PITGSSSTVTVLKVNETPADSALQYTGNIIFTGKLSSETAADSKNLTSKLLQPVTLIS 300

QY      449 GGTLSLKHGVTLOTQAFQADSRLEMDVGTTLPEADTSTINNVINISSIDGAKKAKIE 508
Db      301 GGTLSLKHGVTLOTQAFQADSRLEMDVGTTLPEADTSTINNVINISSIDGAKKAKIE 360

QY      509 TKATSKNLTLSGTITLLDPTGTFYFENHSIRNPQSYDILELKASGTVTSTAVTDPDIMEK 568
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QY 569 FHVYQOTWGPVWGTGASTTATFNWTKTYIPNPERIGSLVPSNLNNAFIDISSLHYLM 628
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QY 629 ETANEGLOGDRAFWAGCAGLSNPFHDKSTKTRGRFHLSGVYVIGNHLHTCSDKILSAAPCQ 688
Db 481 ETANEGLOGDRAFWAGCAGLSNPFHDKSTKTRGRFHLSGVYVIGNHLHTCSDKILSAAPCQ 540
QY 689 LFGDRDRDYFAKNOG--TVGGTGLYYQHNETYIS-----LPCKLR-PCSLSYVP 734
Db 541 LFGDRDRDYFAKNOQSLRSLRRNSLLPAQRNLYLSLQTTALFVLCYSYRSDCSLFRKP 597

RESULT 2
US-09-198-452A-470
; Sequence 470, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-470

Query Match 40.6%; Score 1940; DB 4; Length 930;
Best Local Similarity 43.7%; Pred. No. 1.4e-138;
Matches 416; Conservative 165; Mismatches 324; Indels 48; Gaps 17;

QY 1 MKSSPPKFFVSTFAIPPLSM--TAT---ETVLDSASFQGNKNGFVRESQEDAGTYILF 56
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QY 57 KGNVLTENIPGTGTAITKSCFNNTKGLDTPFTNGNSLLFQTVDAVAGAAVNSVVDKS 116
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QY 117 TPIGFSLSFIASPOSSITGKAVSCSTGSLTKVNSLLSKNFSTD---NGGALTA 173
Db 119 LTFTGFSNLFIAPAGTTVASGKSTLS-SAGALNLTNGTILFSQVNSNEANNNGALTA 177

QY 174 KTLSLCTTMSALFSENTSKKGAIOQSDALITITGNOGVSFSDNTSSDSGAAIFTEAS 233
Db 178 KTLISGNTSSITFTNSAKLGLGAIYSSAAISIGNTGQVFPNNKGETGGGALGFAS 237

QY 234 VTISNNAKVFDINKVTGASSTTGMDSGGAICAYKSTDTKVTLTQNMQLLSNNITSTT 293
Db 238 SSITQSSSLFFSGNTADAAG-----KGAIIYCEKGETPTLTISGNKSLITFAENSST 291

QY 294 AGGAIYVKLELAGGGLTLFSRNVNGTAPKGAIAIEDSGELSLSDSGDIDVFLGNTV 353
Db 292 QGGAICAHLGLDLSAAGTTLFSNNRCGNTAAKGAIAIADSGSLSANQGDITFLGNTL 351

QY 354 TSITT-PTGNRSSIDLGTSAKWTALRSAGRAIYFDPI---TTGSSTTTVDLVKNETPA 409
Db 352 TSTSAPTSTRNAILYGSKATITNRAQQGSIYFDPIASNTTCAS---DVLITNQPDS 407

QY 410 DSALQYTGNIITFTGKLESEPAADSKNLTSLKLOPVTLSGGLSLKHGVTLOQAFQQA 469
Db 408 NSPLDYSCTIVFSGEKLSDAEKAAADNFTSLKQPLASGTLAKGNVELDVNGFTQTE 467

QY 470 DSRLEMDVGTILEPADTSTIN--NLVINISSIDGAKKAKIETKATSKNLTSLGTTILDP 527
Db 468 GSTLLMQPGTKLK-ADTEAISLTILVDLSALEGKNSVSIETAGANKITILTSPLVFQDS 526

QY 528 TGTFFYENHSLRNPOSYDILELKAS-----GTVTSTAVTPDPIMGEKPHYGYQGTWG 578
Db 527 SGNFYEGHTTINQAFQTQPLVWFTAATAASDIYDALLTSPVQTPEP-----HYGVQGHWE 580

QY 579 PIWGTGASTTATFNWTKTYIPNPERIGSLVPSNLNNAFIDISSLHYLMETANEGLQD 638
Db 581 ATWADTSTAKSGTWTWTTGYNPNPERRASVVPDSLWASFDTIRTLOQIMTQANSIYQQ 640

QY 639 RAFWAGCAGLSNPFHDKSTKTRGRFHLSGVYVIGNHLHTCSDKILSAACOLFGDRDRDYEV 698
Db 641 RGLWASGTANFHHKDSGTNOAFRHKSYGYIVGSAEDFSENIQSVAFQFGKDKDLFI 700

QY 699 AKNOQTVGGTGLYYQHNETYISLCKLRPC--SLSYVTEIPVLPSGMLSYTHTDNDLKT 756
Db 701 VENTSHNYSALYLRHRAFLGGLP---MPSTGSIYDMLKDIPLIILNAQLSYKYTKNDMDT 757

QY 757 KYTTVPTVKGSGNDSPALEFEGGRAPICL-DESALFEQYMPFMKLOFYVAHQEGKQGT 815
Db 758 RYTSYPEAQQSGWNNSGALGLGSLALYLKPEAPFFQGYFFELKFQAVYSROQNFESGA 817

QY 816 EAREFGSRLVNLALPIGIRDPKESDCQDAYNLTGYTVDLVRSNPDCITTLRISGDSW 875
Db 818 EARAFFDDGDLVNCSPVIGIRLEKISEDEKNNFELSLAYIGDYVRKNPRTSLMVGASW 877

QY 876 KTFGCTNLARQALVLRAGNHFCFNSFEAFSOPFELGSSRRNRYNDLCAKYQF 928
Db 878 TSLCKNLARQAFASAGSHLTLSPHVELSGEAAAYELRGSALYINVDCCGLRYSF 930

RESULT 3
US-09-198-452A-472
; Sequence 472, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 472
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; NAME/KEY: SITE
; LOCATION: 1...927
; OTHER INFORMATION: Xaa-unknown or other
US-09-198-452A-472

Query Match 40.2%; Score 1917.5; DB 4; Length 927;
Best Local Similarity 44.8%; Pred. No. 7.2e-137;
Matches 427; Conservative 147; Mismatches 328; Indels 51; Gaps 22;

QY 1 MKSSPPKFFVSTFAIPPLSM-----IATETVLDSASFQGNKNGFVRESQEDA-GTT 53
Db 1 MKSSLHFLISSLSLALPLSLNFSAAVVEINLGPNTSPSG--PGTYTPPAQTNAQGTI 58

QY 54 YLFGKGVNLTENIPGTGTAITKSCFNNTKGLDITFTNGNSLLFQTVDAVAGAAVNSSVV 113
Db 59 YNLTGVDVSIYN-AGSPALTATSCKETTNLSFGHGYQFLLQNIADAG--ANCTFTNTAA 115

QY 114 DKSTFTTIGFSSLSFIASPGSSITGKAVSCSTGSLTKVNSLLFKNPNSTONGALTA 173
Db 116 NKLLSFGSFSYLSLIQT--TNATTGTGAIK-STGACSIQSNYSYCFQGNFNDNGGALQG 172

QY 174 KTLSLTGTWMSALFSENTSKKGAIOQSDALITITGNOGVSFSDNTSSDSGAAIFTEAS 233
Db 173 SSISLS-LNPNLTITAKNATOKGALYSTGGITINVLINSASFENPANNNGALYTEAS 231

QY 234 VTISNNAKVSIIDNKVTGASSSTTGMDSGGAICAICYKSTDTTKV-TLTQNMQLLSNNITST 292

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Db      232  SFISSNKAISFINNSVTATSA-----TCGAIYCSSTSAKPVLPLSDNGELNFGNTAI 285
Qy      293  TAGGAIYVKLELASSGLTLFERNVNGTAPKGAIAIADSGELSLSDADSDIVFLGNT 352
Db      286  TSGGAIYDNLVLSGGPTLFKNNSAIDTAAPLGAIAIADSGLSLSDALGGDITFEGNT 345
Qy      353  V---TSTPTGPNRSIDIG-TSAKMTALRSAGRAIYFYDPTTGGSTTVTDVLKVNTP 408
Db      346  VVGASSQTTRNSINIGNTNAKIVQLRASQGNITYFYDPTTITSITAALDNLNPGD 405
Qy      409  ADSALQYTGNIIFTEGKLESETEADSKNLTSLKLPVTLSSGTLKHGVTILOQAFQO 468
Db      406  LAGNPAVQGTIVFGEKLESEAEADNLKSTIQOPLTAGGQLSLKSGVTLVAKSFQS 465
Qy      469  ADSLEMDVGTTLBPADTSTINNLVINISSIDGAKAKIET-KAT--SKNLTLSGTLILL 525
Db      466  PGSTLLMDAGTTLTADGS-----LSIICSQCFLKRDQEXTLKATQASQVTLSSGSLV 521
Qy      526  DPTGTFYENHSLRNPQSYDILELKAS--GTVTSTAVTPDPIMGBKFHYGYQGTWGPVWG 583
Db      522  DPGSNVYEDVSWNNPQVFSCLTLTADDPANIHIITDLAADPLEKNPIHWGYQGNWA-LSWQ 580
Qy      584  TGAST---TATENWTKGYTPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLOQDRA 640
Db      581  EDTATKSKAAILTWKTYGPNPERRGTLVANTLWGSFVDVRSIQQIVATKVRSQETR 640
Qy      641  FWCAGLSNFFHKDSTKTRRGRHLSGGYVIGGNLHTCSDKILSAFQOLFGRDRDYFAK 700
Db      641  IWCEGISNFFHKDSTKINKGRHISAGYVVGATTLASDNLITIAFQOLFGRDRDYFAK 700
Qy      701  NOGTVYGGTLYYOHNETYIISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHDNDLTK 757
Db      701  NRASAYAAASHLOHLATLSS-----PSLLRYLPGSESEQVPLFDAQISYISKNTMKY 754
Qy      758  YTYPTVTKSGWGNDSFALEFGGRAP-ICLDSEALFEQYMPFMKLOFYVAHQEGFKQOTE 816
Db      755  YTOAPKGESSWYNDGCALELASSLPHLTALESHEGLFHAIFYFFIKVEASYIHQDSFKERN 814
Qy      817  -AREFGSSRLVNLALPIGIRFDKESQDQATYNTLGYTVDLVRSNPDCTTLRIISGDSW 875
Db      815  LVRSFSDGDLINVSVPIGITFEFRSNERASYATVIYVADVTRKRPDCTTALLINNTSW 874
Qy      876  KTFGTHLQAQVLRAGNHFCFNSPEAFSQFSFELRGSSRNYNVDIGAKYQF 928
Db      875  KITGTNLRSQAGTGRAGIFYAFSPNLEVTSLNLSMEIRGSSRSYNADLGGKFQF 927

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RESULT 4

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US-09-198-452A-478
; Sequence 478, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE OF INVENTION: 9710-003-999
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 478
; LENGTH: 949
; TYPE: PRN
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...949
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-478

```

Query Match 38.9%; Score 1856; DB 4; Length 949;
 Best Local Similarity 42.7%; Pred. No. 3.5e-132;

```

Matches 405; Conservative 171; Mismatches 331; Indels 42; Gaps 20;
Qy      1  MKSFPKVFVFTFAIPP--LSMIATETVLDSASFDGN-KNGNFSVRSEQEDAGTYYLTK 57
Db      22  MKTIPMWLVSVLAFSCHLQSLANEELSPDDFNGNIDSGTFTPKTS---ATTYSILT 77
Qy      58  GNVLTLENIPTGTALTSCFNNTKGDLTFTGNGSLLPQTVDAGTVAGAAVNSVVDKST 117
Db      78  GDVFYB-PGKGTPLSDSCFQKQTTDNLTLFLNGHSLTFGFDAGTHAGAAA-STTANKNL 135
Qy      118  TFIQFSSLSFIASPGSSITTCGKAVSGSTGSLSTKTNVLSLFSKNFSTDNGCAITAKTLS 177
Db      136  TFGSFLSLSPDSSTVTTTGGTLS-SAGGVNLENIRKLVVAGNFSTADGAKGASFL 194
Qy      178  LTGTTMALSENSTSSKKGAIQTSDALTTTNGNGEVSFSDNTSSDGAALIFTEASVTIS 237
Db      195  LTGTSGDALFSNNSSTKGAIAATTAGAIANNNTGXVFLSNIASTSGAIDDEGTSILS 254
Qy      238  NNAKVSFIDNKVTGASSSTTGDMSGGAIKAYKTSITDTKVTLTGNQMLLFSNNTSTAGGA 297
Db      255  NKRLEYF-----EGNAAKTT----GGAIKNTKASGSPELIISNNKTLIFASNVAETSGA 305
Qy      298  IYVKLELASGGLTLFERNVNGTAPKGAIAIADSGELSLSDADSDIVFLGNTVST- 356
Db      306  IHAKKALSSGGFTFLRNNVSSAT-PKGAIISIDAGSELSSAETGNIIFVRNLTITG 364
Qy      357  TPTGTRSSIDLGTSAKMTALRSAGRAIYFYDPTTGGSTTVTDVLKVNETPADSALOY 415
Db      365  STDTPKENAINISNGKFTELRAAKNHTIFFYDPT--SEGTSSDVLKINNGSAGALNPY 422
Qy      416  TGMNITFTGKLESETEADSKNLTSLKLPVTLSSGTLKHGVTILOQAFQOADSLEML 475
Db      423  QGTILFSGETLTADELKVNADNLKSSFTQPVLSGGKLLLOKGVTLSESTFSQESGSLGM 482
Qy      476  DVGTILE-PADTSTINNLVINISSIDGAKAKIETKATSKNLTLSGTLITLDPGTGYEN 534
Db      483  DSGTTLSTTAGSITIINLGINVDSLGLKQVPSLTAKASNKVIVSGKLNLDIEGNIYES 542
Qy      535  HSLRNPQSYDILELKASGVTS---TAVTPDPIMGEKFHYGYQGTWGPVWGTCGSTT- 589
Db      543  HMFSDQLFLSLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGWNV-VNWTDTATNT 601
Qy      590  --ATFNWTKGYTPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLOQDRAFWCAGLS 647
Db      602  KEATATWTKGYTPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLOQDRAFWCAGLS 647
Qy      648  NPFHKDSTKTRRGRHLSGGYVIGGNLHTCSDKILSAFQOLFGRDRDYFAKNOGTVYG 707
Db      662  NFLHKTGDENRKGFRHTSGGYVIGGSAHTPKDLDLTFEAFCHLFARXKDCFIANNRTYG 721
Qy      708  GTIYYOHNET-----YISL-PCKLRPCSLSYVTEIPVLFSGNLSYTHDNDLTKYTTY 761
Db      722  GTLFFKHSHTLQPNYLRGRAKFSSAEKFPREIPLDALDQVFSFSDNRMETHYTSL 781
Qy      762  PTVKSGWGNDSFALEFGGRAPICL-DESALFEQYMPFMKLOFYVAHQEGFKQGTARF 820
Db      782  PESEGSWSNECIAGGIGLGLDLPVLSNPHPLFKTFIPQMKVEMVYVSQNSFFSSSDGRGF 841
Qy      821  GSSRLVNLALPIGIRFDKESQDQDA-TYNLTLYGYTVDLVRSNPDCTTLRIISGDSWKTG 879
Db      842  SIGRLNLNLSIPVGAKF-VQGDIGDSYTYDLSGFFVSDVYRNNPQSTALVWGPDSWKIRG 900
Qy      880  THLARQALVLRAGNHFCFNSPEAFSQFSFELRGSSRNYNVDIGAKYQF 928
Db      901  GNLSRQAFLLRGSSNNYVYNSNCELFGHVAMELRGSSRNYNVDVGTGLRF 949

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RESULT 5

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US-09-198-452A-474
; Sequence 474, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.

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Tue Aug 17 09:45:49 2004

us-09-428-122-2.ra1

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 474
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-474

Query Match 32.9%; Score 1572.5; DB 4; Length 643;
Best Local Similarity 49.8%; Pred. No. 6.3e-111; Indels 15; Gaps 6;
Matches 314; Conservative 93; Mismatches 209;

Qy 308 GGLTLFSSNVGCTAPKGAIAIEDSGELSLSDSGDIVFLGNVTSTTP-GTNRSSID 366
Db 18 GGGISFNNIVQGITAGNGGALSILAAGECSLSAEAGDITFNGNAIVATTPTQTKRNSID 77
Qy 367 LGTSAKMTALSAAGRAIYFYDDPITGSSSTTVTVLKVNETPADSALOYTGNIIFTGKEL 426
Db 78 IGTAKITNLRAISGHSIFFYDPIANTAADSTDTLNLNKADAGNSTDYSGSIVFSGEKL 137
Qy 427 SETEAADSKNLSKLLQPVTLSSGGLSLKHGVTLOTQAFQOADSRLMDVGTITLEPA-D 485
Db 138 SEDEAKVADNLSTLQKPVTLTAGNLVLRGVTLDTKGTQTAGSSVINDAGTTLKASTE 197
Qy 486 TSTINNLVINISSIDGAKAKIETKATSKNLSLTSITITLDPGTGTFYENHSLRNPQSDYI 545
Db 198 EYTLGLSLPVDLSGEGKVVIAASAASKNVALSGPILLDDQGNAYENHDLGKTQDFSF 257
Qy 546 LELKASGVTSVAVTPDPDPMGKPHFYGYGTGPIW-----GTGASITATTNMTKGYI 600
Db 258 VQLSALGTATTTDPAVPTVATPETHYGYGTGPIW-MTWVDDTASTPKTKATLAWNTGYL 316
Qy 601 NPERRIGSLVPSNLNNAFTDSSHLVLMETANEGLQDRAFWCAGLSNFFHDKSTKTRRG 660
Db 317 PNPERQGPVPSNLNMGFSFSDIQAIQGVIBERSALTCDSDRGFWAAGVANFLDKDKKEKK 376
Qy 661 FRLHSGYVIGGNLHSCDKILSAFQCFGRDRDYFVAKNQGVVGGTLYYQHNNTYIS 720
Db 377 YRHKSGYAIAGGAQTCSENLSISFAFCQFGSKDPLVAKNHTDTYAGAFYIQH-----IT 432
Qy 721 LPOKURPCSLSVYP-----TEIPVLFSGNLSYTHDNDLTKYTYTYPTVKGSGWNSDFALF 777
Db 433 ECSGFTGCLLDKLPGSWSHKPLVLEGQLAYSHVSNLDLTKYTAYPEVKGSGWGNNAFMML 492
Qy 778 GGRAPICLDESALFEQYMPKMQFVVAHQEKFQGTAREFGSSRLVNLALPIGIRFD 837
Db 493 GASHSYPEYLHCFDYAPYIKNLTYIRQDSFEKGTGERSFDDSNLNLPIGVKFE 552
Qy 838 KESDCQDATVNLTYGTVDLVRNPDCTTLRISGDSWKTFTGYNLRAQALVLRAGNHCFP 897
Db 553 KFSDCNDFSVDLTLVYVDLIRNDPKTKTALVSGASWETAYANLARQALQVRAGSHYAF 612
Qy 898 NSNPEAFSPQSFEIRGSSRNVDLGAQYF 928
Db 613 SPMFEVLQGFVEVRGSSRIYNDLGGKQF 643

RESULT 6
US-09-198-452A-15
; Sequence 15, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 15
; LENGTH: 922
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...922
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-15

Query Match 29.7%; Score 1417.5; DB 4; Length 922;
Best Local Similarity 36.5%; Pred. No. 6.4e-99;
Matches 347; Conservative 156; Mismatches 385; Indels 63; Gaps 26;

Qy 5 FPFKVFSTFAIFPLSMIATETVLDDSSASFGDNKNGNFSVRESQBDAGTTLFKGNVTLE 63
Db 8 FPLVFSFTLLSVFDTLSATLITLTPEDSPHGDQN--AERSYNVQAGDVYSLTGDVSI 65
Qy 64 NIPGTGTAITKSCFNNTKGDITFTGNSLLIPQTVDACTVAGAAVNSVVDKSTT-FIGF 122
Db 66 NV--DNSALNKACFPVTSVTFAGNHGXFYFNISGTTKEGAVLCCODPOATARFSGF 123
Qy 123 SLSFIASPGSITTKGAVSC--STGSLSLTKNWSLLFSKNFSTDNGAIKATLSLTG 180
Db 124 STLSPGPGDIKEQG-----CLYSKNALMLNNVVVFEEQNKTKGAISGANVTIVG 178
Qy 181 TTMSALFSENTSSKKGAIQTSDALTITNGQEVFSFNTSSD-SCAAIFTEASVTISNN 239
Db 179 NYDSVSFYQNAAT-FGGAIHSSGPIQIAVNOAEIRFAQNTAKNGSGGALYSDGIDIDQN 237
Qy 240 AKVSFIDNKVTGASSSTTGDMSGGAI CAYKSTDTK-----VTLTGQMLLFSNNTSTTAG 295
Db 238 AVVLFRENE-----ALTTAIGKGAACVCLPTSGSSTPVPVTFVSDNKLQVFRNHSIMGG 292
Qy 296 GAIYVKLELASGGLTLFSRNSVNGTAPKGAIAIEDSGELSLSDSGDIVFLGNVTVS 355
Db 293 GAIYARKUSISSGGPTLFTNNISYANSQNLGGAIALDTGGEISLAEKGTIIFQGN--RT 350
Qy 356 TTPGTNRSSIDLGTSKMTALSAAGRAIYFYDDPITGSSSTTVTVLKVNETPADSALOY 415
Db 351 SUPFLN--GIHLNQNAKFLKQARNGYSIEFYDPIIT--SEADGSTQLNINGPKNK--EY 404
Qy 416 TGNITPTGKLTSEADSKNLSKLLQPVTLSSGGLSLKHGVTLOTQAFQOADSRLM 475
Db 405 TGTILPSGEK--SLANDPRDFKSTIPQNVNLSAGYLVIKEGAETVTSKFTQPGSHLV 461
Qy 476 DVGTTIL-EPADTSTINNLVINISSIDGAKKAK-IETKATSKNLSLTSITLIDPTGTFFE 533
Db 462 DLGTKLIAKEDIATGLAIDIDLSSSSTAAVIKANTANKQISVTDLSIELISPTGNAYE 521
Qy 534 NLSLRNPQSDYIILELK--ASGTVTSTA-----VTPDPIGEKPHYGYGTGPIW-GTG 585
Db 522 DLRMRNSQIFPLSLPEAGGSVTVTAGDFLPVSP-----HYGFGQGNW-KLAWTGTG 572
Qy 586 ASTATFNTTKTYIENPERIGSLVPSNLNNAFTDSSHLVLMETANEGLQDRAFWCAG 645
Db 573 -NKVGEFFWDKINYPKPEKEGNLVPNLMGNVAVDVRSMLQVQVETIASSLQTRGLMIDG 631
Qy 646 LSNFFHKDSTKTRRGPHLSGGVYVIGNLHSCDKILSAFQCFGRDRDYFVAKNQGV 705
Db 632 IGNLFHVSASEDNIRYHNSGGVLSVNNETPKHYTSMAFSOLFSDKDYAVSNNEYRM 691
Qy 706 YGGTLYYQHNET-----YISLPCKLRPCSLSVPTTIP-VLPSGNLSYTHDNDLTKY 758
Db 692 YLGSYLYQYTTSLGNTPRYASRNPVNVGILSRFLQNLPMIFHLFCAYGHATNDMTDY 751
Qy 759 TTPVTVKGSGNUSFALEFGGRAPICLDESA-LPEQYMPKMQFVVAHQEKFQGTGTEA 817
Db 752 ANFPWKNVSRNRCNAIECGSGMPLLVFENGRLPQGAIPFMKLQVLYVAYQGFKEITADG 811
Qy 818 REFSSRLVNLALPIGIRFDFKESDCQDATVNLTYGTVDLVRNPDCTTLRISGDSWKT 877

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      872 RRFSGNSGTSISVPIGRIFREKALASQDVLDFSFYSYIPDIFRKDPSCBAALVIGSDSLV 871
      878 FCTNGLARQALVLRAGNHFCFNFFAFSOFSEFLRCSSRNYNVDLGAKYQF 928
      872 PAHVSRHAFVGSCTGRVHFNDYTELLCKGSEICRPHARNYVINCCKSKEF 922

RESULT 7
US-09-430-723-2
; Sequence 2, Application US/09430723
; Patent No. 6607730
; GENERAL INFORMATION:
; APPLICANT: Murdin, Andrew
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 19721-011
; CURRENT APPLICATION NUMBER: US/09/430,723
; CURRENT FILING DATE: 1999-10-29
; EARLIER APPLICATION NUMBER: 60/106,590
; EARLIER FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/133,071
; EARLIER FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 973
; TYPE: PRN
; ORGANISM: Chlamydia pneumoniae
US-09-430-723-2

```

Query Match	28.9%;	Score 1377.5;	DB 4;	Length 973;
Best Local Similarity	34.8%;	Pred. No. 7.6e-96;		
Matches 350;	Conservative 153;	Mismatches 391;	Indels 113;	Gaps 25;

QY	1	MKSFPKPVST----	FAIPPLSWIATETVLDSSAFDGNKGNFVSRESQEDAGTYYL	55
DB	1	MKTSIRKFLSTLAPCA----	STATFVEIMPSENPFDGSGKIFPYFTTILSDPRGLTLCI	56
QY	56	FKNVTUENIPGTGTAITKSCFNNTKGDLTPTGNGNSLLFQTVDAGTVAGAAVNSVVDK	115	
DB	57	FSGDLYTIANLDNAISRSTSSCFNSRACALQILGKGVFSLNI--RSSADGAAISSVITQN	115	
QY	116	----STTFICGFSSLSF-----	IASPGSITTCGAVSCSTGSLTKVNSLLFSKNFS	164
DB	116	PELCPLSFGSFGSQMIFDNCESLSTDSASNIVPHASAIYATPML--FTNDSILFQYNRS	174	
QY	165	TDNGGALTAKTILSTGTTMGALPSENTSKKGGAIQTSDALITITNGOGEVSFSD-----	218	
DB	175	AGFGAAIRGTSITIENTKSLFNGNGISNGGALTGSAAILNNSAPVIFSTNATGIY	234	
QY	219	-----NTSSDGAAIPTFASVITSNNAKVSFIDNKVTGASS--	254	
DB	235	GGAIYLTGGSMLTSGNLSGVLVFNNSRSRSGAIYANGNVTFSNNSDUTFQNTASPNLSL	294	
QY	255	-----SITGDMSS--GGAI--C-----	AYKTSIDTKVLTITGNQMLFSNNTSTTAGGAIY	299
DB	295	PATPPPTTPAVTPLLIGYGAIAFCTPATPPPTGVSLTISGENSVTFLENIAEQGCALY	354	
QY	300	VKKLELASGGLTLFRRNSVNGGTAPKGGATAIBDSGELSLASDGDIVFLGN--TVTSTTP	358	
DB	355	GKKISIDNSKSTIFL-----	GNTAGKGAITAPESGELSLASNOQDILFNKNSLITSGTP	409
QY	359	GITNRSSIDLTGSAKMTALRSAGRAIYFYDPIITG--SSTVTVDLVKN--ETPADSALQY	415	
DB	410	--TRNSIHFGKDAKFATLGNTOGYTLIFYFDPIITSSDDLASAAATVVPNPKASADGA--Y	465	
QY	416	TGNIIFTGKLSLSTEADSKNLTSKLLQPVTLTSGGTLISLKHGVTLOTQATQOADSLELM	475	
DB	466	SGTIVFSGETLTATEARTPANATSTLNQKLEGGTLALNGAILNVHNPFTQDEKSVVIM	525	
QY	476	DVGTITLEPADTS-----	TINMLVINISIDGAKKAKIETKATSKNLTLSGTITILLDPT	528

RESULT 8

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US-09-198-452A-468
; Sequence 468, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and
; TITLE OF INVENTION: thereof and uses thereof, in particular f
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6649
; SEQ ID NO 468
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-468

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Query Match	26.4%;	Score 1259;	DB 4;	Length 671;
Best Local Similarity	42.0%;	Pred. No. 4.2e-87;		
Matches 280;	Conservative 130;	Mismatches 220;	Indels 24;	Gaps 15;

QY	1	MKSSFPKFFVFTFAIP-PLSMIAETVTLVDS-ASFQGNKNGNFSVRESQF-DAGTITYLFK	57
DB	1	: : : : : : : : : : : : : : :	60
QY	58	GNVTLENIPGTGPAITKSCFNNTKGLTTCNGNSLLFQTVDACTVAGAAVNSVDVKST	117
DB	61	: : : : : : : : : : : : : : :	120
QY	118	TFIGFSSLSFIASPGSSIT-TQKGAVSCSTGSLSTKNVSLFSPKFNSTDNGCAITAKTL	176
DB	121	: : : : : : : : : : : : : : :	179
QY	177	SUTGTTMSALFSENT--SSKKGAIQTSDALITNGQGEVSFSDNTSSDGAIFAIVASV	234
DB	180	: : : : : : : : : : : : : : :	239
QY	235	TLSNNAKVSPFNKVTGASSSTTGDMSGGAI CAYKTSTDTKVTLTGNQMLLFNSNNTSTTA	294
DB	240	: : : : : : : : : : : : : : :	292

Query Match 25.4%; Score 1214; DB 4; Length 230;
Best Local Similarity 99.6%; Pred. No. 2.1e-84;
Matches 226; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-09-198-452A-30
; Sequence 30, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 30
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-32
; Sequence 32, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 32
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-466
; Sequence 466, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 466
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-466

Query Match 25.2%; Score 1203.5; DB 4; Length 507;
Best Local Similarity 46.9%; Pred. No. 4.5e-83;
Matches 235; Conservative 82; Mismatches 165; Indels 19; Gaps 7;

US-09-198-452A-32
; Sequence 32, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 32
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-32

Best Local Similarity 27.6%; Pred. No. 5.8e-77;
Matches 316; Conservative 133; Mismatches 310; Indels 384; Gaps 24;

QY	1	MKSSPPKFVFSFAIFPL-SMIATETVLDDSSASPDGNKNGN---FVSRESQEDAGTYYLFK	57
Db	1	KXYSFLWLLTSALVFSLHPLMAANDLUSSDNYENGSGSAAFTAKETSASGTTLT	60
QY	58	GNVTLENIPGTCITAIT---KSCFNNTKGDLPTFGNGSNILLFOTVDAGTVAGAANSSVVD	114
Db	61	SDVSITNV-----SAITPADKSCFTWTGGALSVPVGADHSILVLTQTI-ALTHDGAALNNT--N	113
QY	115	KSTTFIGFSSLSPFIASPSSSITTGKAVSCST----GSLSLTKNVLSLLFSKNFSTDGGA	170
Db	114	TALSPGFSSLLIDSAPATISGGKGAI-CVNTTEGGTATFTDNASVTLQNKTSEKDGA	172
QY	171	ITAKTSLTGTMTSALFSENTSSKKGGAIQTSDALTTITNGOGEVPSFDNTSSDSGAIF-	229
Db	173	VSAISIDLAKTYTAALLDQNTSKNGGALCALTNTVOGNSGTVTFSSNTATDKGGIYS	233
QY	230	-----TEASVTISNNAKVSFIDNKVTG-ASSSTTGDM	260
Db	233	KEKOSTLDANTGVVTFKNTAKTAGAWSSDDNLALTGNTQVLFOENKTTSSAQAANPEG	292
QY	261	SGGAICAY-KTSTD-----TKVTLTGQMQLLFSNNTS	291
Db	293	CGBAICCYLATADKTGLAISQNOBMSFTNTTTANGAGIYATKCTILDGNTTLTDFDQNTA	352
QY	292	T-----	292
Db	353	TAGCGGAIYTETEDFSLKSGTGTVFSTNTAKTGALLYSKENSLSLTGNTNLLPFGNKATG	412
QY	293	-----	292
Db	413	PSNSSANOEGCGGAILGFLESASVSTKKGLWIENDENVLSIGNATVSGGAIYATKCALH	472
QY	293	-----	292
Db	473	GNTTLTFDGNTAETAGGAIYETEDFLTGSTGTGTVTFSTINTAKTAGALHTKGNSTFTKNK	532
QY	293	-----	292
Db	533	ALVFGSNSATATATTTDQECGGAILCNISBSDIATKSILTLENBSLSFINNAKRSG	592
QY	293	-----TAGGAIYVKKLELASGGLTLFRNSVNGGTAPKGGAI	329
Db	593	GIYAPKCVISGESINFDGNTAETSGGAIYSKNLSITANGPVSFNWS--GG---KGGAI	647
QY	330	AIEDSGELSLSADSGDIVLGNTVTSTTPGNTSSDDLGTSAKMIALRSAAGRIFYDP	389
Db	648	YIADSGELSLAIDGDITFGNRATEGTSPN--SIHLGAGAKITKLAAAPGHITIFYDP	705
QY	390	IT---TGSSSTVTID-----VLKVNETPADSALQYTMGIIFTGEKL	426
Db	706	ITWEAPASGCTIEBELYNPVKAIVPPPQKGPFIASVPVPVAPANPNPTGTVFSSGKL	765
QY	427	SETEAADSKNLTSLKLQPVTLSGGTILSKHGVTLOTQAFTOQADSRLMDVGTTLPEADT	486
Db	766	PSQDASIPANTTTILNQKINLAGNVVLKEGALQVYSTQQPDSVTFMDAGTTLLETYYY	825
QY	487	ST-----INNLVINISSIDGAKAKIETKATSKNLTLSGTITLLDPTCTFFYENHSLRNP	540
Db	826	NNTDGSIDLKNLSVNLDALDGKRMITAVNSTSGGLKISGDLKFHNNEGSFYDNPGLKAN	885
QY	541	QSYDIILELKA-SGTVTASTAVTPDPIMGEKPFHYGYQTGW--PIVMWGTASATTATFNWTKT	597
Db	886	LNLFPDLLSTSTGVNLDFENPTIPSSMAAPDYGYGSWTLVPKV-GAGGKVTLVAEWOAL	944
QY	598	GXYIPNERIGSLVPNSLWNADFIDISSIHYLMETANELOGDRAFWCAGLSNFPHFKDSNKT	657
Db	945	GXTPKPELRATLVPNSLWAYVNIHSIQEIIATMSDASHPGIWIIGGINAFHQDKOKE	1004
QY	658	RRCFRHLGGYVJGNNLHTCSDKILSAAPCOLFGRDRDYFAVAKNGQTVGGTTYQHNET	717


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; SEQ ID NO 190
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Ch
US-09-620-412C-1

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Query Match 23.6%; Score 1126.5; DB 4; Length 1006;
Best Local Similarity 30.1%; Pred. No. 9e-77;
Matches 303; Conservative 160; Mismatches 372; Indels 171; Gaps 30;

QY	48	EDAGTYYLFGKNVTLLENIPGTTGTAITKSCFNNTKGDLTFTNGNSLLLPQTVDAGTVAGAA	107
Db	47	DPSEGTVPFSAGELTKLNDNSIAALPLSCFGNLLGSPVLGRGHSLTENIRTS-NGAA	105
QY	108	VNSSVVDKSTTFIGESSLSF-----IASPGSITTGKAVSCSTGS	150
Db	106	LSNSAAGDLGFTIEGFKELSFNCNSLLAVLPAATTNKGSTPTTTSTPSNGTIYSKTDLL	165
QY	151	LTKNVSLLFSGNFSDNCGAIIKATKLSLTGTTMSALFSGNTSSKKGGAIOFSDALTITGN	210
Db	166	LLNNEKFSFYSLNVSGDGAIDAKSLTVQGISLKCVFOENTAQADGGACQCVVTSAMAN	225
QY	211	QGEVSF-----SDNTSDS	228
Db	226	EAPTAFAVANVAGVGGGIAAQDGGQGVSSSTEDPVVFSRNTAVEFDGNVARVGGI	285
QY	229	FTEASVTISNAKVSFTDN-----KVTGASSSTTCDM-SGGAICAYK	271
Db	286	YSYQNVAFLNKGLFLNNVASPVIIAAKQPTSGAASNTSNNGYGDGGAI PCKNGAOGSN	345
QY	272	TDTKTLTGNQMLLFNNSTSTAGGAIYVKKLELASGGLTLFSSNSVNGGTPAPKGAIAI	331
Db	346	NSGVSFEDGEVGFSSNVAAGKGAIIYAKLSVANCGPVQFLNIAN-----DGGAIYL	400
QY	332	EDSGELSLSADSGDIVFLGN---TVTSTTPGCTN-----RSSIDIGTSAKMTALRSAAGRA	383
Db	401	GESGELSLSADYGDIIIFDGNLKRKTAKENAADVNGVTVSSQAI SMGSGKITTILRAKAGHQ	460
QY	384	IYFYDPTTTCGSTT---VTDVLKVNTPADSALOYTGNIILFTGEKLSFEAADSKNLT	439
Db	461	ILFNDFPIEMANGNNPQAQSSKLLKINDGEG---YTGDIVFA-----NGSS	502
QY	440	KLLQPVTLSGGTLSLKHGVTLOTQAFTQADSRLEMDVGTLE-----PADTS--	487
Db	503	TLXQNVITIEQGRIVLREKAKLSVNSLSQTGS-LYMEAGSTLDPVTPQPQQPFAANQLI	561
QY	488	TINMLVINISSI-----DGAKKAKIETKATSKNLTJSGTTLTLDPTGTFY	532
Db	562	TLNHLHLSLSLLANNVTPNPQAQDSHPAVIGS-TTAGSVTISGPIFFEDLDDTAY	620
QY	533	ENHS-LRNPQSYDILELKASGTVTSTAVTPDPIWGEKF-HYVGQGTWGPVWVGTSATTA	590
Db	621	DRYDNLGSKQKINVKLQOL-GTPEPANAPSDDLILGNEMPKYFGQSG-KLWADPNTANN	678
QY	591	TF---NWTGTGYIPNERTGSIVPNSLMAFIDISLHYLMETANEGLQGRAFWCAGL	646
Db	679	PYTLKATWTKTGNPGPERSVASLPVNSLWGSILDIRSAHSAIQASVDGRSVCRLWVSGV	738
QY	647	SNPFPHKDSKTRGFRHLGSGYVIGNHLHCDSKILSAAPCOLFGDRDRYFVAKNQGTVY	706
Db	739	SNFFYHDDRDLAOGYRIYISGYSIGANSYFGS-SMFLGAPTEYFGRSKDYVVCRSNHHAC	797
QY	707	GGTLYYOHNETYISLPCKLRPCSLSVPTTEIPVLFSG---NLSYTHDNDLKTKYITYPT	763
Db	798	IGSVWLSTQAL-----CG-SY-----LFGDAFIRASYFGNQHMTSYTFABE	840
QY	764	VKSGWNDSPALBFGRAPICLDESALF-EQYMPFKLOFVYAHOBGFEQCGTEAREFGS	822
Db	841	SDVRWNNCLAGEIGAGLPVITPFSKLYLNELRPFVQAEFSYADHESFTEEGDQAEAFKS	900
QY	823	SRULNALPIGIRFDEKESCDODATYNLTIGYTVDIRSNPDCTTILURI SGDSWKTPGTNL	882
Db	901	GHLNLUSVPVGWAFDRCSSTHPNKYSFMAAICDAYRTISGTETTLTSHQETWTTDAFHL	960

[illegible]

RESULT 15

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US-09-598-419-190
; Sequence 190, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Schollier, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121-469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 190
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-598-419-190

```

Query Match 23.6%; Score 1126.5; DB 4; Length 1006;
Best Local Similarity 30.1%; Pred. NO. 9e-77;
Matches 303; Conservative 160; Mismatches 372; Indels 171; Gaps 30;

Qy	48	EDAGTTLFKGNVLTLENIPIGTGTATITKSCFNNTKGDGLTFTNGNSLLLFQTVDAGTVGAA	107
Db	47	DPSGTTVFSAGELTKXNLDNLSIAALPLSCFCGNLLGSFTVLGRHSLTFENIRTSI-NGNA	105
Qy	108	VNSVVDKSTTFIFGSSLSF-----IASPGSSIITKGAVSCSTGS-----LS	150
Db	106	LSNAAADGLFTIEGFKELSFNSCNLSLAVPAATNKGSTPTFTTSTPSNGTIYKTDLL	165
Qy	151	LTKNVSLLFKSNFTGDNGGAIKTAKTLSLTGTTMGALFSENTSSKKGGAIOQSDALTITGN	210
Db	166	LLNNEKFSFYNLSVSGDGAIDAKSLIVOGISKLCVFCQNTAQADGGACQVTSFSAMAN	225
Qy	211	QGEVSF-----SDNTSSDS-----	228
Db	226	EAPIAFVANVAVRGCGGIAAQQDQCGVSSSTSTEDPVVSFSRNTAVEFDGNVARVGGI	285
Qy	229	FTEASVTISNNAKVSFIDN-----KVTGASSITGDM-SGGAI CAYK-----TS	271
Db	286	YSYGNVAFLNNGKTLFNNVASPVYIAAKQPTSGQASNTSNNYGDDGGAICPKNGAQAGSN	345
Qy	272	TDTKVTLTGQMLLFSNNTSTTAGAIYVKKLELASGGLTLFSRNSVNGTAPKGGAI	331
Db	346	NSGSVSPDGEVVFSSNVAAGKGAIIYAKKLSVANGCPVQLRNIA-----DGGAIYL	400
Qy	332	EDGEGLSLSDGDIVFLGN---TWIYSTTPTGN-----RSIDLGTSAKMTALBSAAGRA	383
Db	401	GESGELSLSDYGGIIFDGNLKKTAKENAADVNGVTVVSQAI SMGSGGKTTTLRAKAGHQ	460
Qy	384	IYFYDPITTGSSTT---VTDVLKVNETPADSALQYTGNIIFTEKLSLSETAADSKNLT	439
Db	461	ILFNDPIEMANGNNQPAQSSKLLKINDGEG-----YTGDIVFA-----NGSS	502
Qy	440	KLLQPTVLSGTTLSLKHGVTLTQATFTQADSKLEMDVGTLE-----PADTS--	487
Db	503	TLYQNTVIEQGRIVLREKAKLSVNSLSQTGGS-LYMEAGSTLDFVTPPPQPPQPPAANQLI	561
Qy	488	TINNLVINISSI-----DGAKKAKIETKATSKNLTLSGTLTLLDPTCTFY	532
Db	562	TLNLHLHLSLLANNVTPNPPAQDSHPAVIGS-TTAGSVTISGPIFFEDLDDTAY	620
Qy	533	ENHS-LRNPQSVDIELKASGTVTSTAVTDPDIMGKPF-HYGGQTGWGPTVWGVTGASTTA	590
Db	621	DRYDVLGNSNQKINVLKLOI-GTKPPANASDLTLGNEMPKYGYOGSW-KLAWPNTANNNG	678

Tue Aug 17 09:45:49 2004

QY	591	TF----	NWTKGTYPNPRIGSLVPSLWNAFIDISSLHYLMETANEGLQGDRAFWCAGL	646
Db	679	PYTLKATWTKTGYNPGPEVVASLVPSNLWGSILDIRSAHSAIQASVDCRSYCRGLWVSGV	738	
QY	647	SNPFHKDSTKTRRGERHLSGGYVIGGNLHTCSDKILSAAFCQLFGDRDRDYFAKNQGTYY	706	
Db	739	SNFFVHDDRDLGQGYRYISGGYSLGANSYFGS-SMFGLAFTFVFGRSKDYVVCRSNHHAC	797	
QY	707	GGTLYYQHNETYISLPCKLRPCSLSYVPTEIPVLFSG--NLSYTHTDNDLTKYTTYPT	763	
Db	798	IGSVYLSLSTQQAL-----CG-SY-----LFGDAFIRASYGFGNQHMKTSYTFAE	840	
QY	764	VKGSWGNDSFALEFGGRAPICIDEHALF-EQYMPFMKLQVYVAHQEGFKEQGTAREFGS	822	
Db	841	SDVRWNNCLAGEIGAGLPVITPCKLYLINELRPFVQAEFSYADHESFTEEGDQARAPKS	900	
QY	823	SRLVNLALPIGIRFDKESDQDATYNLTLGYTVDLVRSNPDCTTILIRSGDSWKTFGTNL	882	
Db	901	GHLNLSVPVGVKFDRCSTHPNKYSFMAAYICDAYRTISGTETTLSSHQETWTDDAHL	960	
QY	883	ARQALVLRAGNHCFNSNFEAFSQSFELRGSSRNYNVDLGAKYQF	928	
Db	961	ARRGVVVRGSMYASLTSNIEVYGHGREYRDASRGYCLSAGSKVRF	1006	

Search completed: August 10, 2004, 13:15:24
Job time : 26 secs